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                                                                                       October 1, 1999, 15:32:18 ; Search time 1619.02 Seconds (without alignments) 3751.894 Million cell updates/sec
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           GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                           679419 seqs, 1590154680 residues
                                                                OM nucleic - nucleic search, using sw model
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1: 9b_bal:*

3: 9b_bal:*

4: 9b_ov:*

5: 9b_ph:*

7: 9b_pl:*

10: 9b_pri:*

10: 9b_pri:*

11: 9b_pri:*

11: 9b_pri:*

12: 9b_ro:*

13: 9b_ro:*

13: 9b_ro:*

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15: 9b_ro:*

16: 9b_un:*

17: 9b_un:*

18: em_hum:*

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10: em_hum:*
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em_hum4:*
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                      Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description
1 144.8 7.6 93695 7 ATF2009 AL021749 Arabidops

ACO06585 Arabidops X02741 Rat mRNA fo ACO0748 Arabidops M18340 Rat tyrosin X2520 Human mRNA X5520 Human mRNA X5520 Human mRNA X5520 Human mRNA X55675 H.sapidops ALO1814 Arabidops BD5062 Streptomy L78815 Mycobacteri AJO05198 Streptomy ALO35394 Arabidops ALO2202 Mycobacteri AJO21942 Mycobacteri AJO21841 Mycobacteri ALO21841 Mycobacteri ALO21841 Mycobacteri ALO21897 Mycobacteri L14321 Bovine herp Z95844 Mycobacteri L14321 Bovine herp Z95844 Mycobacteri L14321 Bovine herp Z95844 Mycobacteri L14320 Bovine herp Z95844 Mycobacteri L14320 Bovine herp X4406 Streptomyce AJO04801 Bovine her L14320 Bovine herp X4406 Streptomyce AJO1958 Mycobacte AJO1958 Mycobacte AJO21958 Mycobacte AJO21958 Mycobacte ALO21930 Mycobacte ALO21930 Mycobacte ALO21930 Mycobacte ALO21930 Mycobacte ALO21930 Mycobacte ALO21939 Mycobacte ALO21999 Mycobacte	ALIGNMENTS  ATF2009 93695 bp DNA PLN 27-OCT-1998  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)  92812749 92812474  AL021749.1 GI:2842474  thale cress. Arabidopsis thaliana ELWARYOGA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosidae; Capparales; Brassicaceae; Arabidopsis. Rosidae; Capparales; Brassicaceae; Arabidopsis. Bovan, M., Koetter, P., Hempel, S., Entian, KD., Hoheisel, J., Mewes, H.W., Mayer, K.F.X. and Schueller, C. Uppublished Up
ATACOOG585  2 RNTATRA ATACO07048 RATACO07048 RATATRA COCOTO044 SCHIO HSTYAT ABOO7644 SSCHIO HSTYAT ABOO7644 SSCHIO MTCY279 SAAJ5198 ATVO13 MTVO17 HSBBICP4B MTVO17 HSBBICP4B MTVO17 HSBBICP4B SCT14206 MTVO17 HYVO17 HSBBICP4A SCT14206 MTVO17 HSBBICP4A SCT14206 MTVO17 HSBBICP4A SCT14206 MTVO17 HSBBICP4A SCT14206 MTVO17 MTVO17 HSBBICP4A SCT14206 MTVO17 MTVO17 HSBBICP4A SCT14206 MTVO11 MTVO17 MTVO17 MTVO17 MTVO17 SCCI5 MTVO41 SCCI5 MTVO44 SCCI6 MTVO44 SCCI708 MTVO44 SCCOO7708	ALIGNMENTS  Arr2009 Arabidopsis thaliana DNA chromosome 4 Project) 92842474 AL021749.1 GI:2842474 thale cress. Arabidopsis thaliana Eukaryota: Viridiplantae: Streptophyteuphyllophytes; Spermatophyta: Magnol Rosidae: Capparales; Brassicaceae; Ar 1 (bases It 93695) Brown, M., Koetter, P., Hempel, S., Enti Mewes, H.W., Mayer, K.F.X. and Schuelle Uppublished Uppublish
03495 8 61384 8 61384 18 2754 10 2754 10 2754 10 2754 10 235970 1 235970 1 235970 1 2409 1 25055 1 2764 17 2764 17	93695 bp sthaliana GI:284247 GI:284247 sthaliana viridiplana ytes; Sperrapparales; Cotto:3695, Mayer, K.id to 93695, psis sequeralission Am Klopfetr: Mike Ber
23.252111888884112000.222288004444222222880054444422222288005884444444444	ATF2009 Projector AL021749 92842474 AL021749.1 Linale cress Arabidopsis Eukariotes Eukar
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	REES LOCG LOCG NID NID NID NID NID NID SOUG SOUG SOUG SOUG SOUG SOUG SOUG SOUG

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complement(join(4494. .4666,6567. .6669,6878. .7149,
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COMPLEMENT (4444. . 4666)

// number = 11254
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4987. .504
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kinase lecRK1, Arabidopsis thaliana, PIR2:S68589; Contains
Protein kinases signatures and profile; pos. 328-349 &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(2196. .2578,3325. .3476,4053. .4222))
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Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, E-mail: michael.bevan@bbsrc.ac.uk Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"receptor protein kinase like protein"
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intron

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**trna** 

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cancer were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.orn.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetplantGene (http://www.bs.dtu.dk/netpgene.chspene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.igr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity but with EST similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are predicted by tRNAscan-SE (Sean Eddy, CRNAscan-SE). Simple repeats are hitting by repeatnasker (Arian Smit, http://enome.wustl.cdu/eddy/tRNAscan-SE). Simple repeats are hitting by repeatnasker (Arian Smit, http://enome.appinger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xiaoying Lin
The Institute for Genomic Research
1712 Medical Center Dr.
Rockville, MD 20850, USA
e-mail: xlin@tigr.org
molecular marker mi238
The orientation of the sequence is from SP6 to T7 end of the BAC
Eukaryota, Viridiplantae, Streptophyta, Embryophyta: Tracheophyta; euphyllophytes, Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae, eurosids II; Brassicales; Brassicaceae;
                                                                               Arabidopsis.

1 (bases I to 103495)

1 (bases I to Shea, T.P., Fujii, C.Y., Shen, M., Vanaken, S.E., Kaul, S., Kaul, S., Mason, T.P., Fujii, C.Y., Shen, M., Benito, M., Barnstead, M.E., Mason, T.M., Bowman, C.L., Ronning, C.M., Benito, M., Carrera, A.J., Creasy, T.H., Buell, C.R., Town, C.D., Nierman, W.C., Fraser, C.M. and Venter, J.C.
Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (04-ARR-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Apr 4, 1999 this sequence version replaced gi:4522000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="exon predicted by xgrail, quality excellent" complement(353. .418)
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                                                                                                                                                                                                                                                                                                                         Lin,X. and Kaul,S.
Direct Submission
Submitted (19-FEB-1999) The Institute for Genomic Research,
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
3 (bases 1 to 103495)
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1. 103494
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206. .243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
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100. .136
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/note="exon
                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          964 atcgactcgctggaatccatcgccgacaagaacaccaccgccatggtcatcataaacccc 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    844 geoggegecaacattetgetececaggecaggetacecaaactaegaggegegegegeg 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.1e-09;
0; Mismatches 117; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(11074. .11254)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .10996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          .10604)
                                                                                                                                                                                                                                                                                                                                                     complement(9901. .9975)
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                                                                                                                                                                                                                                                                            .9900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10056. .10127
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complement(10605. .1099
                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(9976.
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                                                                                                                                                                                       complement(7763.
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                                                                                                                                                                                                                                                                      complement(7916.
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                                                                                                        complement(7648.
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Arabidopsis thaliana
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Query Match

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DEFINITION

ACCESSION

ORGANISM

KEYWORDS SOURCE

VERSION

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/ Anote-"excon predicted by xgrail, quality excellent"
12742. .12884
12742. .12884
12742. .12884
12742. .12884
12743. .12886
Complement(12902. .12986)
Anote-"excon predicted by xgrail, quality
Anote-"excon predicted by xgrail, quality
complement(14051. .14971)
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FSPRMVQSPVTSPLPNRSPTQGSPASISRFHSSPSSLGITSILHDHGSCKDEESTSSS
                                                                                     PASPSISFLPTLHPLTSSQPKKASPQCPQSPTPVHSNGPPSAEAAVTSSPLPPLKPLR
                                                                                                           ILSRPPPPPPPPPSPSTRSTPSPSSTSNSIATQGPPPPPPPPPLQSHRSALSSSPLPP
PLPPKKLLATTNPPPPPPPPHSNSRMGAPTSSLVLKSPPVPPPPAPAPLSRSHNGNI
                                                                                                                                                                  PPVPGPPLGLKGRGILQNLKGQGQTRKANLKPYHWLKLTRAVQGSLWAEAQKSDEAAT
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/rpt_family="(TGG)n"
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//note="exon predicted by xgrail, quality excellent"
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0804..10902
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//note="exon predicted by xgrail, quality good"
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11494..1157
//note="exon predicted by xgrail, quality excellent"
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11355..12137
//note="exon predicted by xgrail, quality excellent"
11356..12037
//note="exon predicted by xgrail, quality excellent"
11357..12137
//note="exon predicted by xgrail, quality excellent"
12135..12251
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Pred. No. 2.1e-09;
0; Mismatches 128;
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Best Local Similarity 63.1%;
Matches 219; Conservative
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                                                                                                                            join(1626. .1742,1826. .1889,2061. .2169,2257. .2410,
2506. .2755,2850. .2926,3010. .3062,3149. .3203,3287. .3475)
/gene="F27C12.1"
.2755,2850. .2926,3010. .3062,3149. .3203,
                                                                                                                                                                                                                                                                                                                                                                    DLDDKTSFFGVYDGHGGKVVAKFCAKYLHQQVISNEAYKTGDVETSLRRAFFRNDDMM
QGQRGWRELAVLGDKMNKFSGMIEGFIWSPRSGDTNNQPDSWPLEDGPHSDFTGPTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                              GRINGSLNLTRAIGDMEFKONKFLPSEKOMYADPDINTIDLCDDDDFLVVACDGIMD
CMSSQELVDFIHEQLKSETKLSTVCEKVVDRCLAPDTAIGEGCDNMTIILVQFKKPNP
SETEPEDSKPEPSEDEPSSSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MASSSLHVAIFSLIFLFSLAAANBYTVGGKSGDWKIPPSSSYSF
TEWAQKARFKVGDFIVFRYESGKDSVLEVTKEAYNSCNTTNPLANYTDGETKVKLDRS
GPFYFISGANGHCEKGQKLSLVVISPRHSVISPAPSPVEFEDGPALAPAPISGSVRLG
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FMLASLLLYRKQFSGEHRTLEMIYKQAPRELLQLMSPLNPLPSQLRFLQYISRRNVGS
QWPPLDQALTLDCVULRLIPDFDGEGGRPIFRIYGQDPFMASDRTSKYLFSMPRRSK
AWROYKQAPCELVKIDINCHILGDVVLECTTLGSDLEREEMMFRVYRYTAFLRSNILTI
LNRGEIDVLWNTTDRFPKDFSAEVIFSEMGAGKKLASVDLPHMEEKDVLPMEAFAKVQ
                                                                                                                                                                                                                                                                                                                                              /translation="MGTYLSSPKTEKLSEDGENDKLRFGLSSMQGWRATMEDAHAAIL
                                                                                                                                                                                                                                                                                                                                                                                                                           CTACVALIKDKKLFVANAGDSRCVISRKSQAYNLSKDHKPDLEVEKERILKAGGFIHA
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note="exon predicted by xgrail, quality good"
i777. .5857
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join(7609. 8283,8382. .8603,8902. .10233)
/gene="r27cl2.3"
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/gene="F27C12.2"
/genement(join(4062. .4414,4489. .4666))
/gene="F27C12.2"
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//otce="exon predicted by xgrail, quality 6795. .6873
/note="exon predicted by xgrail, quality
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/note="exon predicted by xgrail, quality
excellent_shadowexon"
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complement(5974. .6004)
/note="exon predicted by xgrail, qu
complement(6006. .6052)
/rpt_family="AT_rich"
complement(6248. .6315)
/note="exon predicted by xgrail, qu
                                                                                                                                                                                                                                     /product-"protein phosphatase 2C"
Protein_id="Anal23006.1"
/db_xref="PID:4559345"
/db_xref="GI:4559345"
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/protein_id="AAD23008.1"
/db_xref="PID:94559347"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="early nodulin 16"
/protein_id="AAD23007.1"
/db_xref="PID:94559346"
/db_xref="GI:4559346"
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/gene="F27C12.3"
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/note="exon predicted"
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.2410,2506.
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                                                 'gene="F27C12.1"
                                                                             1069. .3608
/gene="F27C12.1"
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2506. 2755
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Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                          753
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                                                                                                                                                                                                                                            994 CATTTT--TGGCAATGAGATTCGAGACGGGCTGGTGAAACTGAGTCAGCGGATCCTGGGA
                                                                                                                                                   cacegooggoggacccaggogatcgaggtcataatcccggtgctggcccagaccgccgg
                                                                          cgtggcagagcacctgtcgcagggcgtgccgtacatgctatcggccgacgacgtcttcct
                                                                                                            GGTCGCTTCTTAC - - TACCACTGTCATGAGGCTCCTCTGGAAGCTAAGGATGTCATTCT
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NPCGSVFSKRHLQKILAVAERQCVPILADEIYGDMVFSDCKYEPLANLSTNVPILSCG
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POEFYHDTLSFLKSNADLCYGALAAIPGLOPVRPSGAMYLMVGIEMEHFPEFENDVBF
TERLIAEQAVHCLPATCFEYPNFFRVVITVPEVMMLEACSRIQEFCEGHYHCAEGSGE
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                                                                                            Rat mRNA for tyrosine aminotransferase (L-tyrosine: 2-oxoglutarate aminotransferase EC 2.6.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2362)
Dietrich,J.B., Genot,G. and Beck,G.
Structural and immunochemical properties of rat liver tyrosine
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1 (bases 1 to 2362)
Grange,T., Guenet,C., Dietrich,J.B., Chasserot,S., Fromont,M.,
Befort,N., Jami,J., Beck,G. and Pictet,R.
Complete complementary DNA of rat tyrosine aminotransferase
messenger RNA. Deduction of the primary structure of the enzym
85293103
                                                                            12-SEP-1993
                                                                                                                                                                                                         Norway rat.
Rattus norvegicus
Eukaryota; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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98. 1462
/note="tyrosine aminotransferase (aa 1-454)"
/codon_start=1
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Pred. No. 7e-09;
0; Mismatches 494; Indels
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1. .2622
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                                                                                                                                                                     X02741.1 GI:57327
transferase; tyrosine aminotransferase
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2345. .2350
/note="strong polyA signal"
2362
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Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RW/RepeatMasker.html), Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.
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the submitted sequence, but they appear in the overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xiaoying Lin

When Institute for Genomic Research
9712 Medical Center Dr.

Rockville, MD 20850, USA
e-mail: xlin@tigr.org
molecular marker mi148
molecular marker mi148
The orientation of the sequence is from SP6 to T7 end of the BAC
  euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                             1 (bases 1 to 61384)
Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E.,
Lin,X., Kaul,S., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.,
Carrera,A.J., Creasy,T.H. Buell,C.R., Town,C.D., Nierman,W.C.,
Fraser,C.M. and Venter,J.C.
Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence
                                                                                                                                                                                                                                                                                   Lin.X. and Kaul.S.
Direct Submission

Direct (09-MRR-1999) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org

3 (bases 1 to 61384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-MAR-1999) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Mar 25, 1999 this sequence version replaced g1:4389529. Address all correspondence to:
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/rpt_family="AT_rich"
697. .721
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384. And
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/rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                        (bases 1 to 61384)
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EDDGDEDDNNNNSEDNKAFWGEHEQLLQGTLYRTSSIETKIRQATKEALKOYKSKGLY
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1423. 1572
/note="exon predicted by xgrail, quality excellent"
complement(1528. 1620)
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/rpt_family="AT_rich" 5283. .5408
                                                                complement(1528. .1520)
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//note="exon predicted by xgrail, quality
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complement(7723..7789)
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837. .6880
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                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:4512647"
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231. .7292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="POLY_A"
3837. .3973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F23N11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Draft entry and computer-readable sequence for [1] kindly submitted by J.L.Hargrove, 07-NOV-88.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Biemann, K.
The structure of tyrosine aminotransferase: Evidence for domains involved in catalysis and enzyme turnover
J. Biol. Chem. 264, 45-53 (1989)
                                                                                                                                                                                                                                          to mRNA, clones pcTAT[1-4].
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                                                                                                                                                                                                                                                                                    Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Mammalia,
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 2004)
Hargrove, J.L., Scoble, H.A., Mathews, W.R., Baumstark, B.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 CAACATGAAGGTGCAGCCCAATCCGAACAAGACCGTGATTTCTCTGTCAATTGGGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="tyrosine aminotransferase (EC 2.6.1.5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 131; DB 12; Length 2
Pred. No. 1e-07;
0; Mismatches 500; Indels
                                                                      Rat tyrosine aminotransferase mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                              tyrosine aminotransferase.
Rat (adult Wistar) hepatocyte, cDNA
Rattus norvegicus
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49.18;
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Best Local S
Matches 493
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KEYWORDS
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                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                      REFERENCE
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                                                            RATTATRA
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join(10040. 10154,10340. 10507,10608. 10936,11019. 11237)
/gene="F23N11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD21704.1"
/db_xref="PID:q4512649"
/db_xref="G1:4512649"
/translation="MTLLVYKGAAKVSIVMIGQQAIMDSYLCLLHLTAGILVESLFNA
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                                    quality good_shadowexon"
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                                                                                                                                                                                      good
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="exon predicted by xgrail, quality excomplement(9912 .. 9988)
/note="exon predicted by xgrail, quality marginal shadowexon"
join(<10040 .. 10154,10340 .. 10507,10608 .. 11
/10019 .. 11237)
/gene="F23N11.3"
/gene="F23N11.3"
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//note="exon predicted by xgrail, quemarginal_shadowexon"
9666. 9814
//note="exon predicted"
complement(7930. .8000)
/note="exon predicted by xgrail, qu
8174. .8302
/note="exon predicted by xgrail, qu
complement(8455. .8586)
/note="exon predicted by xgrail, qu
8702. .8829
/note="exon predicted by xgrail, qu
8702. .8829
/note="exon predicted by xgrail, qu
8702. .8829
/note="exon predicted by xgrail, qu
8704. .9051
/note="exon predicted by xgrail, qu
8936. .9051
/note="exon predicted by xgrail, qu
9147. .9243
                                                                                                                                                                                                                                                                                                                                                                          /note="exon predicted by xgrail, quego, 9390. 9338 complement(9317. 9461) /note="exon predicted by xgrail, quego, 9555 complement predicted by xgrail, quego, exon predicted by xgrail, quego, exon predicted by xgrail, que
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Pred. No. 2.1e-08;
); Mismatches 123;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. Actinomycetales; Streptomycineae; Streptomyces. I (bases 1 to 39524)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABC transporter; adenylosuccinate synthetase; aspartate aminotransferase; ATP-dependent profease ATP-binding subunit; cytochrome P-450 hydroxylase; fba; fructose 1,6-bisphosphate aldolase; lipase/esterase; oxidoreductase; purA; RNA polymerase sigma factor; spermidine synthase; transmembrane efflux protein; two-component regulator; two-component sensor kinase; uridine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1052 CCATGC-ACCATAGTCCAGGGTGCTCTGAAGAGCATCCTTCAGCGAACCCCTCAGGAGTT 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1111 CTATCACGACACGTTAAGCTTCCTCAAGTCCAATGCGGACCTCTGCTATGGGGCCACTGGC 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1449 ggaaaacaaatacattacatgtcctcacaagccagaaggatcaatgtttgtcatggtgaa 1508
                                                                                                                                                                                       1029 cccgtgccgcagcgtttactcctacgaccatctgtccaaggtcgcggaggtggcgaaaag 1088
                                                                                                                                                                                                                                                                                   1089 gotoggaatattggtgattgotgacgaggtatacggcaagctggttctgggcagcgccc 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       994 CATITIT -- GCCAATGAGATTCGAGACGGCCTGGTGAAACTGAGTCAGCGGATCCTGGGA 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1171 TGACCTCCCTGGACTCCAG---CCGGTCCGCCCTTCTGGAGCCATGTACCTTATGGTGGG 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          874 ATACGAACCACTGGCCAACCTCAGCACCAATGTTCCCATCCTGTCCTGTGGTGGGCTGGC 933
                                                                                                                                       ACAACTGGAATCTCTGATCGATGAAAACTGGAATGTCTTGTTGTCAACAACCCATCCAA 753
caggetggaggteeggeatttegaeeteateeegaeaaggggtgggagategaeatega 968
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                           754 TCCCTGTGTGGCTCCGTGTTCAGTAAGCGACACCTTCAGAAGATTTTTGGCAGTGGCTGAAAG
                                                                                                                                                                                                                                                                                                                  ctcgctggaatccatcgccgacaagaacaccaccgccatggtcatcataaaccccaacaa
                                                                                                                                                                                                                                                                                                                                                                                   gttcatcccaatgggagtgtttgggcacatcaccctgtgctgtccatagggtctctgtc
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Unpublished
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      correct initiation codon. Where possible we choose an initiation codon (atg, gr, trg or (att)) which is preceded by an upstream initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If the cannot be identified we choose the most upstream initiation codon. If the because we only sequence sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid HIO lies between 6513 and H44 on the Asel-H genomic
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FGNPYLCDFLHRLRVQSWVCTVQHLRRLSELRGALWSGHTALVDALARRDVPGARALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SCH10.01"
hypothetical protein, partial CDS, len:
>19 aa; probable CDS suggested by positional base
preference, GC frame analysis and amino acid composition"
                                                                                                          project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="overlap with S.coelicolor cosmid St66T3 from 35058
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                Submitted (05-MAX-1999) Streptomyces coelicolor sequencing proj Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBBO 18-A E-mall: barrellGeanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                     Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
3 (bases 1 to 39524)
James,K.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
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/protein_id="CAB42010.1"
/db_xref="PID:01428991"
/db_xref="PID:94753847"
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/transl_table=11
/label=SCH10.01
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/gene="SCH10.01"
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/gene="SCH10.02"
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33805 GCGACCTGCTGGTGGTGACCGACGACGACTACGAGCACCTGGTCTTCGGCACCGCCGAGC 33864
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llarity 50.2%; Pred. No. 8.5e-07;
Conservative 0; Mismatches 345; Indels 6
                                                                                                                                                                                                                                                               complement(2749. .3240)
/gene="SCH10.06c"
/note="SCH10.06c, hypothetical
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complement(2749. .3240)
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                                                                                                                     HLGPSLLLATGVLWPPGIVLVR
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/label=SCH10.06c
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DGRRTALLVFDWQDSSQMPPICEPFLMEINAEVDLCPIMNGDDLAKGLSQLG"
complement(1472...2356)
/gene-"SCH10.04c"
/note-"SCH10.04c, probable RNA polymerase sigma factor,
/note-"SCH10.04c, probable RNA polymerase sigma factor,
sige, Mycobacterium avium extraorycphasmic function
alternative sigma factor (251 aa), fasta scores; opt: 226
z-score: 266.2 E(): 1.6e-07, 29.8% identity in 168 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MRSPLLACDLWLVPLVDVLCHTPDNPFAEELAQYDKVLAEAGLP
PVPVYQYMPGLSGEVAPVAGFDYDALHFLRRAHLLQVGGLPVTPVDELGGDYEQLLEM
FESTAQOSHLVWHYDHAGAYVPVDFPHPLSSDELLAGGGPLGSSHTLLRELEAVAPAL
GIDPANPPAPPQPPLAPTELEEPAVPAPHDSSPFARERHVWLGLHAAATRSLAQGSMI
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complement(1143. .1433)
/gene="SCH10.03c"
/note="SCH10.03c"

P="SCH10.02, hypothetical protein, len: 221 aa; pwn function, probable CDS suggested by positional preference, GC frame analysis and amino acid
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unknown function, probable CDS suggested by positional
base preference and GC frame analysis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"hypothetical protein"
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                                                                                                                                                                                                                                                                                        /label-SCH10.02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:94753848"
/db_xref="GI:4753848"
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/gene="SCH10.05c"
complement(2472. .2672)
/gene="SCH10.05c"
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/codon_start=1
/transl_table=11
/label=SCH10.04c
                                                                                                                                                                                                  /codon_start=1 ·
/transl_table=11
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/label=SCH10.03c
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IVYL
translation="MTDRYSAASCQGPYGGENGPEDCGDPVRFEVARHLRAPLRVCPV"
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                                                                                                                                                                                                                          /note="SCH10.06c, hypothetical protein, len: 163 aa;
unknown function, probable CDS suggested by positional
base preference, GC frame analysis and amino acid
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/gene="SCH10.07c"
/opene="SCH10.07c"
/gene="SCH10.07c, purA, probable adenylosuccinate
/note="SCH10.07c, purA, probable adenylosuccinate
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KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
 BASE COUNT
ORIGIN
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NPCGSYFSKRHLQKILAVAARQVPLILADEIYGOMYESOKYBPLALTSSTDPRILSGG
GLAKKLYPEWRLGWILIHDRRDIFGNEIROGLYKLSGRILGECTIVQGALKSTILCRT
PGEFYHNTLSFLKSNANLCYGALAAIPGLRPVRPSGAMYLMVGIEMEHFPEFENDVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSDMAKKTFNPIRAIVDNMKVKPNPNKTMISLSIGDFTVFGNLPTDPEVTQAMKDALD
SGKYNGYAPSIGFLSSREEIASYYHCPEAPLEAKDVILTSGCSQAIDLCLAVLANPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MDPYMIQMSSKGNLPSILDVHVNVGGRSSVPGKMKGRKARWSVR"
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                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (08-MAR-1990) Scherer G., Institute of Human Genetics,
Albertstr 11, D 7800 Freiburg
9bases 1-2754)
                                 33865 ACATCCCCCTGGCGTCCTTCCCGGGGATGCGGGAGCGCACGGTGACCATCGGGTCGGCCG 33924
 1151 tcatcccaatgggagtgtt---tgggcacatcaccctgtgctgtccatagggtctctgt 1207
                                                                                                                                                                               HSTATR 2754 bp mRNA PRI 12-SEP-1993
Human mRNA for tyrosine aminotransferase (TAI) (EC 2.6.1.5).
X52520
                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 2754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="placenta (genomic) and liver (cDNA)"
/clone_lib="genomic (phage) + cDNA"
                                                                                                                                                                                                                                                                      X52500.1 GI:36712
aminotransferase; transferase; tyrosine aminotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="genomic (phage) + cDNA"
/clone="lambda-hTAT1, phcTAT2-16 + phcTAT3a-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="tyrosine aminotransferase (AA 1-454)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rettenmeier, R., Natt,E., Zentgraf,H. and Scherer,G. Isolation and characterization of the human tyrosine aminotransferase gene aminotransferase gene Nucleic Acids Res. 18 (13), 3853-3861 (1990)
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/note="direct repeat flanking Alu element"
2783. .2743
/note="major mRNA polyadenylation signal"
2754
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Moote="minor mRNA polyadenylation signal"
2090
                                                                                                     33925 GCAAGACGTTCTCGTTCACCGGCTGGAAGGTCGGCTGGGTCACCG 33969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Data kindly reviewed (26-JUL-1990) by G. Scherer.
Location/Qualifiers
                                                                         1208 ccaagtcatggatagtgcctggatggcggcttggatgggtagcgg 1252
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Anote="datact repeat flanking Alu complement(2131. .2479)
Anote="Alu element"
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2116. .2130
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/db_xref="SWISS-PROT:P17735"

    .2754
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="16q22.1"

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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2051)
Labrio.F.

Labrio.F.

Direct Submission
Submitted (26-SEP-1990) Labrie F., CHUL Research Centre, Laboratory
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                                                                                                                                                                                                                           371 AAGTTACCCAGGCAATGAAAGATGCCCTGGACTCGGGCAAATATAATGGCTATGCCCCAT
                                                                                                                                                                                                                                                                                                             431 CCATCGGCTTCCTATCCAGTCGGGAGGAGTTGCTTA---TTACCACTGTCCTGAGG
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    Length 2754;
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H.sapiens mRNA for tyrosine aminotransferase.
X55675
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Score 118; DB 10;
Pred. No. 3.3e-06;
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      Query Match 6.2%;
Best Local Similarity 50.1%;
Matches 348; Conservative
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NILVPRPGESLYKTLAESMGIEVKLYNLLPEKSWEIDLKOLEYLIDEKTACLIVNNPS
NPCGSVFSKRHLØKILAVARQCVPILADEIYGDMVFSDCKYEPLATLSTDVPILSCG
GLAKRUVPGWRLGWTLINDRRDIFGNREIRDGLVKLSGRILGFCTIVOGALKSTILCRP
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      Sainte-Foy Quebec
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of Molecular Endocrinology, 2705 Blvd Laurier, Sainte-Foy Quebk GlV 462, Canada 2 (Dases 1 to 2051) Seralini, G.E., Luu-The, V. and Labrie, F. Gloning and expression of human tyrosine aminotransferase CDNA Biochim. Biophys. Acta 1260 (1), 97-101 (1995)
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Pred. No. 3.5e-06;
0; Mismatches 340; Indels 6
                                                                                                                                                                                                                                                                                                                                  /product="tyrosine aminotransferase"
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                                                                                                                                                                                                                                      Lot # 2102"
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/dev_stage="adult"
                                                                                                                                                                                                                 /tissue_type="liver"
/clone_lib="# HL1001b.
/clone="B1"
/map="16q 22.1"
                                                                                                                                                                                                                                                                                   .1415
_number="2.6.1.5"
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Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N.
and Tabata,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB007644 73840 bp DNA PLN 13-FEB-1999
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17,
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                                                                                                                                          1121 acggcaagctggttctgggcagcgcccgttcatcccaatgggagtgtttgggcacatca 1180
                                               tgtccaaggtcgcggaggtggcgaaaaggctcggaatattggtgattgctgacgaggtat 1120
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DNA Res. 4 (6), 401-414 (1997)
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                                                                                                                                                                                                                                              TTCAGAAGATTCTGGCAGTGGCTGCACGGCAGTGTGTCCCCCATCTTAGCTGATGAGATCT
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53.8%; Pred. No. 2.4e-06;
tive 0; Mismatches 217;
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/db_xref="taxon:3702"
/chromosome="5"
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/note="SC2H4.02, unknown, len: 2183; very limited similarity to proteins of the RHS family e.g. WAPA_BACSU
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/protein_id="CAA20595.1
/db_xref="PID:e1319219"
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/gene="SC2H4.01"
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/qene="SC2H4.02"
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Parkhill, J., Barrell, B.G. and Rajandream, M.A.

Direct Submission

Submitted (01-SEP-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK

3 (bases 1 to 25970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor.
Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinopacterides;
I (bases 1 to 25970)
Oliver, K. and Harris, D.
Unpublished
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50937 TTTATCACATCGGGTTGCACGCAAGCGATCGATGTAGCATTGTCGATGTTAGCTCGTCCC 50996
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A set of ordered cosmids and a detailed genetic and physical may
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                                                                       50997 A---GGGCTAATATACTTCTTCCAAGGCCTGGTTTCCCAATCTATGAACTCTGTGCTAAG
                                                                                                                                                 964 ategactegetggaatecategeegacaagaacaecegeeatggteateataaaeeee
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                                                                                                               ttcaacaggctggaggtccggcatttcgacctcatccccgacaaggggtgggagatcgac
                                     51174 GGTAATCCTTGCGGGAATGTCTATAGCTACCAGCATTTGATGAAGGTTAGCTTTAAACTT
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beta-mannosidase; sugar transport system; sugar-binding
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11. Microbiol. 21 (1), 77-96 (1996)
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Streptomyces coelicolor cosmid 2H4.
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Kroph et al., Nucleic Acids Research, 22(22):4766-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
in/cgi-bip/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most upstream initiation codon.

IMPORTANT This sequence MAY NOT be the entire insert of the sequenced chone. It may be shorter because we arrange for a small overlap between neighbouring submissions. Cosmid 244 lies between 265 and AHIO on the Asel-B genomic restriction fragment.
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SAFTLYYSASYKKWYFNRTAGDVKDRPVYLRSCIGDATAPPLKWTHLAAVFDDTKRDTN
KNDTIQLFVUGRPQGEPVVLDGVSTAYQPWVSSGCLQIGRSLVGGAWGEHFRGRLDE
VNWWQRYLTPDEITQQAQLLEEGYPANELVAQWDAASSTGTTVKELSSYPAPSLTLSA
AGAVLDEENNALVLDGSAGYASATGPVVDETGSFTVSARVQLDSAKLASKPVGYEALV
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DTDITGYRWRLLTTSAKEAKAVTGKSVTVSDVTPSLSGTQVLSVEAKDVRSRWGAPAE
FSFKVAPAAGATGTWHFDDALPGSGVTIAKDTAAEGTRHDATLYTAGAGWSTLARRGD
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VTGVFDAQEPWEWTDPADSAKTETRYGRLHLYVGEFDQPSETASGFTTPQYGAGALAV
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CDS, len: >606 aa; contains PS00017 ATP /GTP-binding site
                                                                                      (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PS00017 ATP/GTP-binding site motif A (P-loop)" 1949. .1953
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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/db_xref="GI:3559957"
/db_xref="SPTREMBL:086584"
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Matches 362;
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DOSIMILER KHTGKRGTOLSLDAVKEHVENDINTUNGORDDILLSFERPRIETVVSETG
AQTIVDYLPADCVAGOTMPKADENBERCFPYWSPGGEEPILDBFGKYPYSSYRTTD
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LPADAARPGDVVSDKATAYDTTTWSATQKPTKGDRWSGRAKGYGGDDRFLWQTTAVT
DYDTLGRRYQYRNTDDYTTSKTENQPPAAGPLTSTTVVNAKGHRTTTVKDFALGADLK
VDANGKVTESAYDSLGRVTSWTENYDPRAGSTATVNAKGHRTTTVKDFALGADLK
VDANGKVTESAYDSLGRVTSWTRYNGARJAKTVYGTSYKGTSLPWTSADALD
DGSGRATYR ITDSLLEFRRQVOADSAGGGRVLAQILLYDGRGLPVTRQADIUNDTAAPA
GGSTRTYR ITDSLLEFRRQVOADSAGGGRVLAQILLYDGRGLPVTRQADIUNDTAAPA
GRIVQLDGGGARPRYDSAGGYDGRACHVENYRAYTKEYGTENTAAATTYDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGRQVSVTDPDKGTTVTEYDALDRAVKSTDGRGEVLLFEYDVLGRKTGMWQSAKTGAN
KLAAMSPDILAKGOODTAVRYBGGEGEORAYTGYRYDDLYKTVNDELTLPANDDLVA
AGVPARLAFGTGY MLDGTVKGAAPAVAGLSAETVSYTYDGLGOVLTAKGTTGYLOQA
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BOANTISVSDATTLGGTGKANYYLNNDYEAGTRRLTRSYVTDGHGEMLQELKYQQD
PAGNITSVSDATTLGGTGKANHQCFYTYDGHRALESAMTPETACSTSGRYVAGLGGAA
PYWTSYQYDDSGLRSKQTEHBASGDDVTTEYRGTARGOPHALSATYTGAENGSYTYD
ETGNTETRFGVRATQTLDWNAEGRLAGVSEPAAGGKPATGTAVYDAGGDLLIRRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDGETVLYLGTTEVHLKVSGNGAAKALSGARTYKAGSAVIAVRTSTAGVSGTKLTFLA
GDHHGTSGLAINADTLAFAKRWSTPFGAPRGTASGAWPDDRGFLGKPADAATGLTQLG
ARQYDPDTGRFLSVDPLLEPDKPNTLNGYAYASNSPVTNSDFSGTSDGLGGLLGAIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIGGVVGAVIGAVGAAITAVGSLGGGGGGGWGGTAPTSSGGWTQPLTKQWTPGATVNF
ITKSWDLPFNPPSQSLEEMLASMPDWGIVSDPKAANRWETSRSLFFGWLWGGGYPLRE
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YKFNSLRGAAKDIAGVLTNGAVGTGNOADAFLGTYSGKARISSINKKEGSVTLKFSAW
NGSDWRSATHVVPRSWNPAFEDTFGAAVREDFSWEEKWPINECVNYSEWLE"
wall-associated protein precursor (2334 aa), fasta scores; opt: 141 z-score: 206.8 E(): 2.7e-09, 23.4% identity in 137 aa overlap, and RHSA-ECOLI RHSA protein precursor (1377 aa), fasta scores; opt: 135 z-score: 222.4 E(): 3.8e-05, 23.0% identity in 1016 aa overlap. Contains possible membrane anchor around aa 1900. Alternative start
                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:086585"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGTSWPTAGSARLTASGGAADEAAPGRLPVTLAPPAAKKAKRADRVKVDVLDQKAARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGVKGVVLKVTGPADGGAARLGIDYSAFAAAYGGDWAGRLQVLRLPDCTTACPPATPV
KFTNERGDERLIADLAFAPKAASGQTWTLALAAGTASADGDYKAIPLAPSSTWEAGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGSFTWSYPLKAPEPAAGEAPKLEISYDSGSVDGRTSTSNNQGTEVGEGFDITSSFIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GADNGDDNGEYWTVTTGDGTREVFGONKLDGAAADVRTKSWWTVPVFGDDEGEPGYAD
GTGFTSRDEKGAWRWIDJAAEDTHGWATTWYTBEDTNWTVLGDDDTGTSYRGGYLK
GIGFTSRDRAGALESGTPGASHRIVLGHDERCLASGTGCDALTEDTRDNWPDVPDRICK
DGDKCPYLDSPSFFTRKMLISVSTYAWDAAAATPAFSPVDTWTLEHLYLDPGGTGDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKYGSCTDDGHADRHDLCWKYDNASLVLNGKATELVKDDTTGQWRLKNDDASKVTHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contains possible N-terminal signal sequence with appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SC2H4.03, possible lipoprotein, len: 153 aa;
                                                                                                                                                                                   aa 27 would give N-terminal signal sequence"
                                                                                                                                                                                                                                                                                /product="hypothetical protein SC2H4.02"
/protein_id="CAA20596.1"
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/note="hairpin loop with 17/17 bp stem"
8602. .9063
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/gene="SC2H4.03"
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/transl_table=11
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'gene="SC2H4.03"
                                                                                                                                                                                                                                                            /transl_table=11
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stem\_loop

gene CDS

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complement(9074. .10282)
/gene="SC2H4.04c, probable aminotransferase, len: 402 aa;
smilar to many e.g. AAT_BACST aspartate aminotransferase
(EC 2.6.1.1) (393 aa), fasta scores; opt: 657 z-score;
(607.8 E(): 1.38-26, 33.9% identity in 386 aa overlap.
Contains Pfam match to entry PF00155 aminotran_1,
Aminotransferases class-I, score 136.00, E-value 6.9e-37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10214 CGCCAACGCGCTGGAGGAGGCGGGGCACAGCGTGCTGCGCCTGAACACCGGCAACCCGC 10155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cescaasecestecaciacciciecaacaacaacaacaasisataaccceaaccigeccaa 9810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9983 ceccercresascrearcrecarecerecaecercrecrecreassa...---cecca 9930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggcagagcacctgtcgcagggcgtgccgtacatgctatcggccgacgacgtcttcctcac 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane lipoprotein lipid
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RSGSEIGLSFAEQSDEPCRLTLTVVDDGDTLCATSDPETPCDLGVRFTRKD"
8647. .8679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552 cgcgagcgtgcaggagaagggccgcggccgtgctgccgctggccacgggggacccgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10043 CGCCCAGCGCTACCAGGCGCTCGGCCTGGAGGTGGACGTGGACGTCTTCCTGGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 cgtgttcccggccttccgcacggccgtcgaggccgaggacgccgtcgccgccgcgtgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 112.4; DB 1; Length 25970;
Pred. No. 9.7e-06;
0; Mismatches 341; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 25970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative aminotransferase"
/protein_id="cAA20598.1"
/db_xref="PID:e1319222"
                                                                               /note="PS00013 Prokaryotic me
attachment site"
complement(9074. .10282)
/gene="SC2H4.046"
complement(9074. .10282)
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                             8647. .8679
/gene="SC2H4.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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ilarity 50.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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'n

Fri Oct

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clone:MAB16.
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophyta; Spermatophyta; Magnoliophyta; eudicotyledons; coreeudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
         9374
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                                                                                                                                                                                                                                                                                                                                                                                          9254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5, Pl clone: MAB16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (06-OCT-1998) to the DDBJ/EMBL/GenBank databases.
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan (E-mail:Ypakamu@kazusa.or.jp, Tel:+81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9073 CAATTGCGCCTGATCTACTGTGCTTGACCTTCAACGGTCTTTCGAAAGCCTACCGTGTCG 9014
                                                                                                                                                                     865
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                                                                         749 agggogtgocgtacatgotat---cggcogacgacgtottcotcaccgcoggoggacoc
                                                                                                                                                                                                                                                                                                                                                                                                                               cogacaagaacaccaccgccatggtcatcataaaccccaacaaccgtgcggcagcgttt
                                                                                                                                                                                                                                                                            926 atttcgacctcatccccgacaaggggtgggagatcgacatcgactcgctggaatccatcg
                                                                                                                                                                                                                                                                                                                                                                                 9313 ATTACCTCTGCGACGAAACCCAAGGCTGGCAACCAGATATCGCCGACGTGGAATCTAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          9193 ACAGCAACGAAATCCTTAACCAAATAGTCGACCTAGCACGTAAGCATCAGCTGCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1166 tgtttgggcacatcacccctgtgctgtccatagggtctctgtccaagtcatggatagtgc
                                                                                                                    9492 IGGICGACGGGIICCCCCCGATICGACGICGATGACGICIAICICGGCAACGGCGICICCG
                                                                                                                                                              806 aggogatogaggtoataatocoggtgotggcocagacogocoggogocaacattotgotoo
                                                                                                                                                                                                       9432 AGCIGATCACGAIGACGCIGCAGGCCCIGITAGACAACGGC-GAICCAAGGIGCIGAICC
                                                                                                                                                                                                                                                     ccaggccaggctacccaaactacgaggcgcgcgcgcgttcaacaggctggaggtccggc
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Arabidopsis thaliana genomic DNA, chromosome
complete sequence.
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2 (bases 1 to 70475)
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Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae
MAD1. Microbiol. 7 (2), 197-206 (1993)
93188700
                                                                                                                                                                                                                                       Mycobacterium leprae (clone: cosmid B1970) (tissue library: Lorist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please contact Doug Smith rmation. The sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated by the Genome Sequencing Center at Genome Therapeutics Corporation (Collaborative Research Division),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the presence of a Shine-Dalgarno sequence, or overlapping orf tha suggested translational coupling. It is possible that the actual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (Dases 1 to 39399)
Smith, D.R., Richterich, P., Rubenfield, M., Butler, C., Lee, H.-M., Xu, O., Gunderson, K., Chung, M., Maher, J.K., Deloughery, C.,
Aldrich, T., Imrich, J., Tulig, C., Smyth, A., Drill, S., Avruch, A.S.
Rice, P., Abendschan, K., Aldredge, T., DeLoughery, C., Kirst, S., Safer, H., Connelly, S., McDougall, S., Eiglmeier, K., Bergh, S., Prepublication submission
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence may not represent the entire cloned insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differs from the one selected.
Lostion/Qualifiers
1.39399
//Organism="Mycobacterium leprae"
//organism="Mycobacterium leprae"
//obst="leaxon:1769"
//clone="cosmid B1970"
//tissue_lib="Lorist 6"
//note="The liver of the armadillo was used to isolate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insert of a Lorist 6 cosmid clone from a mapped set of clones constructed from M. leprae genomic DNA isolated from armadillo
9569 GACGIACCGGGIGGCGGGITICCGCICCGGCIGGTGGTGGTGACGGGGCCGAAGCAG 9512
                                                                                                                  26-JUN-1996
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                                                                                                                                                                                                                                                                              Mycobacterium leprae
Mycoteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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51.8%; Pred. No. 1.3e-05;
live 0; Mismatches 275; Indels
                                                                                              MSGB1970CS 39399 bp DNA BCT
Mycobacterium leprae cosmid B1970 DNA sequence.
L78815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beaver St., Waltham, MA, 02154. Please co (smith@cric,com) for further information.
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Best Local Similarity 51.83
Matches 300; Conservative
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thaliana"

 .70475
 /organism="Arabidopsis /strain="Columbia"
 /db\_xref="taxon:3702" Location/Qualifiers

source

'n

Gaps

4;

689 gctacccgccggcgtcggcctccccgccgcagaagcgccgtggcagagcactgtcgc 748

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FEATURES

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/EC_number="2.6.1.1"
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/gene="SecE"
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 7409)
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Submitted (22-MAY-1995) to the DDBJ/EMBL/GenBank databases.
Yasuhiro Yamada, Osaka University, Department of Biotechnology;
Yamadaoka, Suita, Osaka 565, Japan (Tel:06-879-7431,
Fax:06-879-7488)
                                                                                                                                                                                                                                     59787 AGGGCTGTTGCAGAGTACCTCTAGTGATCTCTCTTACCAGATATCAAATGATGTT 59728
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                                                                                                                                                                  Gaps
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/organism="Streptomyces virginiae"
/db_xref="taxon:1961"
                                                                                                                              DB 7;
                                                                                                                                                                0; Mismatches 138;
                                                                                                                             Score 110.2; DB 7
Pred. No. 1.4e-05;
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 /chromosome="5"
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23859 a 11672 c 11571 g 233
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complement(98. .1117)
/gene="ada"
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Unpublished (1995)
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TREKKARKGGKRGKKGPLGRLALFYRQIVAELRKVVWPTRNQLTTTTVVIVFVVIMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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/YEARAAILDPGDEVYYPAPWYHYPEPSIRLAGGVPVDVADETTGYRVSCBOLEAART
/*ERRAYULFVSPSNPTGSVYSEADAKAIGEWAAEHGLWWLTDEIYEHLVYGEAKFTSLP
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DPTSYAPLLGGMIPAVPALILDAVDAASRETGLGMRYLIAARRHKHPLDARTLARLAVR
SARGIVGFGCLSNDERRGMRDFDRAFAIAREGGLLAAPHGGELTGPSSVRDCLDDLH
ASRIGHGVRAAEDPRLKRLADRQITCEVCPANVALGSYBREDVPERTLEREGVBAN
ALGADDPLLFGSRLAAQYEIRHAFTDTELAELARGSVRGSAAPDDVQAKLLAGID
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ALAAVSGNLDAVAEMRKAFDRRQTMVKMLNEIDGVFCPTPEGAFYAY PSVKELLGKE
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Query Match
Best Local Similarity
Matches 317; Conserv
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MTCY279/c
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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I (bases 1 to 9150)

Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeler,K., Gas,S., Barry III,C.E.,
Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
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Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
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                                                                                                                                            2502 CACCCTCGCCGTGGACGCCAAGGCCCTCAAGGCCGCCGGCGGCGCCCGGTGATCGG
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                                                                                                                                                                                               ggacccgtccgtgttcccggccttccgcacggccgtcgaggccgaggacgccgtcgccgc
                                                                                                                                                                                                                                                                                          663 cgccgtgcgcaccggccagttcaactgctaccccgccggcgtcggcctcccgccgcacg
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                                                                                                caagatcagcgcgagcgtgcaggagaaggggccgcggccgtgccgctggcccacgg
                                                                                                                                                                                                                                            2442 CITCGGTGCCGGCGAGCCCGACTTCCCGACCCGGACTACATCGTCGAGGCGGCGGTCGA
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
     Length 7409
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                                                     Indels
                                                  0; Mismatches 334;
     Score 103.6; DB 1 Pred. No. 0.00014;
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5.48;
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/note="Rv038c, (MTCY279.05c), len: 882, unknown iron-sulfur protein, first of several possible start sites chosen. Some similarity to other hypothetical proteins eg. YWJF_BACSU P45866 hypothetical 79.2 kd protein in acda (705 aa), fasta scores; opt: 1188 z-score: 894.6 E(): 0, 34.8 identityin 682 aa overlap. Contains PS00070 Aldehyde dehydrogenasescysteine active site and two of PS00198 4Fe-4S ferredoxins, iron-sulfur binding region signature"
                                                                                                                                                                  /note="Rv0337c, (MTCY279.04c), len: 429.aspc, aspartate aminotransferase, similar to many eg. TR:048143 (EMBL:032823) aspartate aminotransferase (404 aa), fasta scores; opt: 1646 z-score: 2132.9 E(): 0, 57.2% identity in 404 aa overlage, also some similarity to M. tuberculosis protein MTCY06G11.12 (27.2% identity in 383 aa overlagh)"
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PYIGRWDALGFLQDFFATAVFLGITTFAIIRILRNPREIGRSSRFYGSHNGGAWLVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDLARKHQLLLLADEIÍDKÍLYDDAKHISLASIAPDMLCLTFNGLSKAYRVAGYRAGW
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/gene="Rv0338c"
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                                                                                      complement(1771. .3060)
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                                                                                                     CDS
                                                                                                                                                                                                                                                                                                           Direct Submission Submitted on behalf of the Mycobacterium Submitted (11-JUW 1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique Moleculaire Bacterianne, Institut Pasteur. 28 rue du Docteur Roux, 75724 paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced 91:2276330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQLVALGELFAYRWSRCGGREEWVMDTWAAVAAEVAAALRISOGLAASRLRYARAMRE
RLPKTAEVFSAGDIGYLMFATIVYRTDLIVDPDVLAAVDAQLAANVARWPSWTKARLA
GQVDKIVARADADAVRRRKEYQAQRQFWVGESQDGVCQIGGSLLAVDAHALDARLSAL
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VRCRDLTCRWPGCDEPATNCDLDHTIPYAAGGPTHASNLKCYCRTHHLVKTFWGWRDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Wodel of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLPDGTLILTSPSGHTYVSTPGSALLFPSLCHFSGGIPAPEADPPYDHCDQRTAMMPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
Barrell,B.G. Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence Nature 393 (6685), 537-544 (1998)
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                                                                                                                                                           Erratum:[[published erratum appears in Nature 1998 Nov
12;396(6707):190]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'possible RBS upstream of Rv0336"
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/strain="H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="H37Rv"
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1. .9150
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REMARK
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                                TITLE
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HLLISGWIKMOEGQLESASADYAAASAGTHLIRRDALWAAALOTAISRRTGDIGALQQ
HWYAAMEALAEYSLDLFALLPLGELWYAAARWRQVDQLQHTLDQALTLLDSIGANPALW
SNSLHWAGVHAGILANSPESVAPHGQALGAWYAHSTLAQALSDAGRTWAKVLAENVDA
DEVTRAARSLSHVGITSDATRLAQDTGSDARYSGAMLQJARDLKLGNDFGEPPSG
AGDTEPASGTPPAPRQPPAGSPLSDRRREVAELLLLGMPYRDIGARLFISAKTVEHHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFLIHAVSARAQAPAQAAKVALIERLRRLDEPTLDTILMMSLTHELGYSDVAAALGIS
VTDARGLVDRAHASGLIESSHTAAFLQSVHDATAQIVGNAHHHEVETSLLRSQLDISP
VSAELALRLAEHGLRDERLADILTRYAADTRDASVRCARLYRAAVHAGAKGLTVRLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALARTGOCTAAATLADDLLSSPDATERAAAVRVAASVAVHDGNTGHAAELFGWLGPHP
DTMVSSAATIVFAANGDLATARATLRLKDAGPPTMAARCARNLAEGLLLTMDQPYPVA
MAKLGQAIATEQSLSQVIPDSPAALVTLAAIHAGDPVRARSVIGRAVRAGADPLFQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MOHRGCKNRGQAYDASVTDSLTEVPPAARRALLELANAPTVPVK
VLITGGIGTGKTTYLAAARDTLRRSGLTVLACPPPDGEPPETALVIDDAQLLTDTELL
RLTERVADSRLTVVAAAEAREHHRALRALTMALERDRPRISLGPLPVAEHLRDCTAGL
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                                                                                                                                                                                                               /note="Rv0339c, (MTCY279.06c), len: 832 aa; unknown, some similarity to a hypothetical protein from streptomyces TR:055102 (EMBL:13457) CHO-ORF3 (883 aa), fasta scores; opt: 168 z-score: 267.2 E(): 6.1e-08, 25.5% identity in 812 aa overlap. Contains PS00017 ATP/GTP-binding site motif A (P-loop)"
4Fe-4S ferredoxins, iron-sulfur binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2789 GGTACTCCGACTCGCAGGCCATCCTGTCGGCCCGGCGTGCGGGTGCTCACGCGCTACGAGC 2730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCGAAATCCTCACCCAGATGGTCGATCTGGCCCGCAAGCATCAACTGCTGCTGTTGG 2370
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/db_xref="PID:e330323"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:033269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="PID:g2276336"
/db_xref="GI:2276336"
                                                                        complement(5848. .8346)
                                                                                                                                              complement(5848. .8346)
/gene="Rv0339c"
                                                                                                       /gene="Rv0339c"
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APDAPEVRLALDAOTCVAVSRGELTVGEGVRAGRIELSGEGTLARALLAT"
                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces anulatus abacteria; Actinobacteridae; Bacteria; Flrmicutes; Actinobacteria; Actinomycetales; Streptomyciaee; Streptomyces. 1 (bases 1 to 3240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (04-JUN-1998) Jimenez A., Universidad Autonoma de Madri
Submitted (04-JUN-1998) Jimenez A., Universidad Autonoma de Madri
Scaultad de Ciencias, Centro de Biologia Molecular 'Severo Ochoa'
(CSIC/UAM), Cantubblanco. Madrid, 28049, SPAIN
2 (bases 1 to 3240)
Tercero,J.A., Espinosa,J.C. and Jimenez,A.
StgR, a new Streptomyces alboniger member of the LysR family of transcriptional regulators
  TCGCCCCGGAIAIGTTGTGCCTGACCTTCAATGGGCTGTCGAAGGCCTACCGCGTCGCCG 2250
                                                                                                                                                                                                                                                                                                                           LysR-type transcriptional regulator; stgA gene; stgR gene; stgU
                                                                                                                                                                                                              04-SEP-1998
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                                                                           GATACCGGGCCGGCTGGCGATCACCGGACCCAAGGA 2209
                                                                                                                                                                                                         3240 bp DNA BCT alboniger stgA, stgU and stgR
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Search completed: October 1, 1999, 15:34:36 Job time: 6179 sec

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4.5 Compugen Ltd. GenCore version Copyright (c) 1993 - 1998

nucleic search, using sw model OM nucleic

October 1, 1999, 15:35:15 Run on:

; Search time 148.69 Seconds (without alignments) 3213.847 Million cell updates/sec

US-09-026-400-3 Perfect score: Sequence:

IDENTITY\_NUC Scoring table:

311585 seqs, 125096042 residues Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. N\_Genesed\_36:\* Database :

	Description		Nicotianamine amin Dendomising oligon	Mandomising Oligon POR brimer for 5'	`.≓	M. tuberculosis im	Mycobacterium tube		DhpA-mel chimeric	Homo gantone mamma	Human adenosine Al		E C	Platenolide syntha	Platenolide syntha	ycobacterium t	. tuberculo	Streptomyces venez	groEL-1 gene codin	gro es el operon w	groen-1 gene. Reco		Mycobacterium spec				Streptomyces roseo	ycobacterium to	M. tuberculosis im	Brn-sa polynucieot	Klanouin receptor	Total DNA Sequence	ycobacterium tu	M. tuberculosis im	. aurectaciens	M tuberculosis im	roel-1 deno nar	gion of S.	T.F.	ion.
SUMMARIES	ID	814	V4614/	036859	V44439	V64548	T93610	T61454	T61455 V05372	V13836	X53491	X53491	T93610	T78508	T80414	V44424	V64533	T68715	022482	022484	V22483	743231 737348	0474CV	X34250	T71711	T93095	V25925	V44433	V04042	010612	Q10013	TOTOTO	V44439	V04048	01100	V64546	022481	046806	T59268	076213
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Claim 4; Page 14-15; 17pp; English.

The nicotianamine aminotransferase can be used in a plasmid to transform plant cells to produce cells with enhanced iron absorption, and it is implied [though not stated] that plants with improved resistance to iron deficiency chlorosis in calcareous soils can be regenerated from the transformed cells. The gene fragment can be used to detect, amplify and/or isolate nicotianamine aminotransferase genes.
Sequence 1910 BP; 462 A; 534 C; 546 G; 368 T;
R. sphaeroides Adh
Rhodobacter sphaer
                                                                                                                                                                                                                                                                                                                                                          protein, gene.
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Nicotianamine aminotransferase 58148.62 molecular weight prods; nicotianamine aminotransferase; plant; iron absorption;
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/product= "Nicotianamine transferase"
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                                                                                                                       ALIGNMENTS
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19-EEB-1998; 102891.
21-FEB-1997; JP-037499.
(SUMO ) SUMITOMO CHEM CO LTD.
MOTI S, MARANIShi H, Takahashi M;
PP-PSDB; W61643.
   V62125
V64112
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Gramineae sp.
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                                               tacaagatcagcgcgagcgtgcaggagaaggggccgcgggcccgtgctgccgctggcccac
                                                                          cgaagcgccgtggcagagcacctgtcgcagggcgtgccgtacatgctatcggccgacgac
                                                                                                                                                                   gcgttcaacaggctggaggtccggcatttcgacctcatccccgacaaggggtgggagatc
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                           541 TACAAGATCAGCGCGCGAGCGTGCAGGAGGGGCCGCGGGCCCGTGCTGCCGCTGCCCCAC
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Claim 4; Page 12-13; I7pp; English.

The nicotianamine aminotransferase can be used in a plasmid to transform plant cells to produce cells with enhanced iron absorption, and it is implied (though not stated) that plants with improved resistance to iron deficiency chlorosis in calcareous soils can be regenerated from the transformed cells. The gene fragment can be used to detect, amplify and/or isolate nicotianamine aminotransferase genes.

Sequence 1660 BP; 423 A; 442 C; 430 G; 365 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotianamine aminotransferase 49564.15 molecular weight protein, geneds; nicotianamine aminotransferase; plant; iron absorption;
 ATGGTGAAACTGAACTTACATCTTTTGGAGGAAATAGACGATGACATTGATTTTTGCTGC 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 gaggactccgcgcgacgacggcgagagcaacgggcatgcggcggcggcggcagaggaggag 456
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                                          tttagttctctatgaatagaagtcaacatctccttgaatagttctggttgttgtgggct
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                                                                                    aaatcattctgtcaaaggaacaagaagaagaaattcgagcgatgattgctagttgtatatc
                                                                                                                                                                                                                                                                                    TITAGITCTCIATGAATAGAAGICAACAICICCTIGAATAIGITCIGGITGITGIGGCCT
                             aagctcgcaaaagaagaatcagtaatcttatgcccagggaagtgttcttggaatggcaaac
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                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Nicotianamine aminotransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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19-FEB-1998; 102891.
21-FEB-1997; JP-037499.
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		577 cggcccgtgctgccgctggcccacggggacccgtccgtgttcccggccttccgcacggcc 636	637 gtcgaggccgaggacgtcgccgccgccgccgcaccggccagttcaactgctacccc 696 	697 gccggcgtcggcctccccgccgcacgaagcgccgtggcagagcacctgtcgcagggcgtg 756 	757 cogtacatgctatcggccgacgacgtcttcctcaccgccggcgggacccaggcgatcgag 816 	817 gtcataatcccggtgctggcccagaccgccgccaacattctgctccccaggccaggc 876 	877 tacccaaactacgaggcgcgcgcgttcaacaggctggaggtccggcatttcgacctc 936 	937 atccccgacaagggtgggagatcgacatcgactcgctggaatccatcgccgacaagaac 996 	997 accaccgccatggtcatcataaaccccaacaacccgtgcggcagcgtttactcctacgac 1056 	1057 catctgtccaaggtcgcggaggtggcgaaaaggctcggaatattggtgattgctgacgag 1116 	1117 gtatacggcaagctggttctgggcagcgcccgttcatcccaatgggagtgtttgggcac 1176 	1177 atcaccctgtgctgtccatagggtctctgtccaagtcatggatagtgcctggatggcgg 1236 	1237 cttggatgggtagcggtgtacgacccagaaagatcttacaggaaactaagatctctaca 1296 	1297 tcaattacgaattacctcaatgtctcgacagacccagcaaccttcattca	1357 cctcagattcttgagaacacaaaggaagatttctttaaggcgattattggtctgctaaag 1416 	1417 gaatcatcagagatatgctacaaacaaataaaggaaacaaatacattacatgtcctcac 1476 	1477 aagccagaaggatcaatgtttgtcatggtgaaactgaacttacatcttttggaggaaata 1536 	1537 gacgatgacattgatttttgctgcaagctcgcaaaagaagaatcagtaatcttatgccca 1596 
d y	<b>Q</b>	QQ Dp	oy Op	Q7 Q0	OY DD	CY Pp	QZ Dp	Qy Qu	Qy	QY Dp	QY Db	Qy Db	60 Pb	QY Db	Qy Dp	Qy Db	Qy Db	δλ

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Example: Page 55: 102pp; English.

Example: Page 55: 102pp; English.

The sequence is that of an example randomising oligonucleotide which is used in the prepr. of markA encoding candidate polypeptides for the method of systematic polypeptide evolution by reverse translation (SPERT). The method provides a rapid way of isolating and identifying polypeptide ligands which bind to target mols. The polypeptide ligands can be used in e.g. assay methods, diagnostic procedures, cell sorting, as activators or inhibitors of target mol. function, as probes, as sequestering agents, drug delivery vehicles, modififers of hormone action and as catalysts. See also Q21830-Q21832.

Sequence 390 BP; 125 A; 126 C; 133 G; 6 T;
                                                                                                             1716
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                                                                                                                                                                                    1717 agcgatgattg------ctagttgtatatctgactgagctgtaaatcat 1760
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 CATGACGACATAGATTTTTGCTGCAAGCTCGCAAAGGAAGAATCAGTAATTTTATGTCCA 1312
                                                                                                                                                                                                                                                                                                                                                                              1553 TGTCCAAGTCATGTACTCTACTTTTGATGTATTTGGCCTCATTGCCTTGCATTGCATTTC 1612
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                                                                                                                                   gggagtgttcttggaatggcaaactgggtccgcattacttttgcttgtgttccatcttct
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by reverse translation; SPERT;
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Systematic polypeptide evolution by reverse translation; SPERT # ligand binding; ss.
Synthetic.
N W09202536-A.
D 20-FEB-1992; UG5463.
F 02-AUG-1991; UG5463.
A (COLS ) UNIV OF COLORADO.
A (COLS ) UNIV OF COLORADO.
I Gold L, Tuerk C;
N WPI: 92-080018/10.
T New method of systematic polypeptide evolution by reverse translation - by linking each polypeptide in sample mixt. to individualised mRNA allowing further synthesis of selected
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Matches 312;
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SEAROPIE 1; Page 84; 98pp; English.

SPERT is used to select novel polypeptides that bind the antibody

of the epitope commonly recognised by the antisera from autoimmune

mice which are the f1 progeny of a cross of NZB and NZW parents

(Portanova et al., J. Immunol. 144, 4633, 1990). The known epitope

consists of ca. 10 amino acids at the N-terminus of the histone HZB

protein. To make mRNA encoding candidate polypeptides a 5' fixed

sequence composed of a T7 promoter sequence and a ribosome binding

sequence composed of a T7 promoter sequence and a ribosome binding

sequence composed of a T7 promoter sequence and a ribosome binding

cite which is recognised by both prokaryotic and eukaryotic ribosomes,

terminating in a restriction endonuclease site is synthesised and cloned

using a number of oligonucleotides (example shown). A 3' fixed sequence

terminal trailer sequence of ca. 100 nucleotides lacking stop codons.

In addition, a 3' primer annealing site is provided so that cDNA

ribosome complexes. See also of the mRNA recovered from partitioned

ribosome complexes. See also 125 A; 126 C; 133 G; 6 T;
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CFC primer for 5' fixed sequence contg. T7 promoter and RBS.
Systematic peptide evolution by reverse translation; SPERT; ligand; specific; inhibitors; probes; assay; cell sorting; ss.
                                                                                                                          ccgcgagagcaacggccatgctgaggccgccgacgcgaacggcgagagcaacgagcatgc
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31-JAN-1992; U00801.
31-JAN-1992; US-739055.
(UVRE-) UNIV RES CORP.
Gold L. Pribnow D. Smith JD. Tuerk C;
WPI: 93-076529409.
Systematic polypeptide evolution by reverse translation - used for prodn. of polypeptide ligand specific for desired target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 390;
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New Isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.

To develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.

To also also also also also antique and antiquence portion of Mycobacterium tuberculosis antique x25; 5′ DNA is provided in W4438. XP25 DNA was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using sera from patients having certapulmonary tuberculosis. It bears no similarity to known sequences. The invention relates to methods and compositions for diagnosing tuberculosis. It provides polypeptides (see W64291-W64379) comprising an antique portion of a soluble M. tuberculosis antiqen, or an immunogenic portion of a soluble M. tuberculosis antiqen, or an immunogenic portion of a soluble M. tuberculosis antiqen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic transfected host cells. Also claimed are methods and diagnostic transfected host cells. Also claimed are methods and diagnostic and transfected host cells. Also claimed are methods and diagnostic and transfected host cells. Also claimed are methods and diagnostic and transfected host cells. Also claimed are methods and diagnostic and transfected host cells. Also claimed are methods and diagnostic and transfected host cells. Also claimed are methods and diagnostic and transfer and tr
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tgccgaggccactgcgaacggccacggcgaggccactgcgaacggcaagaccaacggcca 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis antigen XP25 3' DNA.
Tuberculosis; infection; diagnosis; antigen; XP25; ss.
Mycobacterium tuberculosis strain Erdman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       these polypeptides, antibodies or oligonucleotide
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13-MAR-1997; U2-818111.
13-MAR-1997; US-818111.
(CORI-) CORIXA CORP.
Campos-Neto A, Dillon DC, Houghton R, Lodes M.
WPI; 98-251292/22.
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PER 18-APR-1996; DG-107184.

PR 29-APR-1996; DE-017184.

PR WPL; 97-549750/50.

DR WPL; 97-549750/50.

PT used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents

PT vaccination and development of anti-mycobacterial agents

PT vaccination and development of anti-mycobacterial agents

Claim 1: Fig 9; 55pp; English.

C New claimed DNA (A) has one of 3 isolated Mycobacterium

C New claimed DNA sequences of 3946 bp (1) (T93610), 2653 bp (VI)

C (see T9361) or 440 bp (IX) (see T93612), or hybridises to, or is a companion of these sequences. Also claimed are RNA transcripts

CC fA), and proteins encoded by (A). To isolate (I), a cosmid clibrary of M. tuberculosis DNA was screened with degenerate probes

CC (A), and proteins (see W31852-55). These OSFR can be amplified and cloned into vectors for expression in E. coli or other hosts.

CC of a proline-rich protein (See W31851 and W31856-57). The claimed together encode 3 proteins (see W31851 and W31856-57). The claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 CGGGGCCGGCGGGCCGGCGGCAACGCCGCGACGGCGGGGGCGCGCAACCGGTGCCGC 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               539 ACGCGGCAACGCGGGCGTCGGCCTGACAGCCAAGGCCGCGGCGGCGGCGCCGCGGGCA 598
  375 cggcgagagcaacgagcatgccgaggactccgcgggcgaacggcgagagcaac----g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 AGGTCTCGGCGACAACGGCGGGGTCGGCGGTGACGGTGGCGCCGGTGGCGC-CGCCGCA
                                                                             195 ccatggcgtggatgccgacgcgaacggcaagagcaacggccatggcgtggctgccgacgc
                                                                                                                                                                           255 gaacggcaagagcaacggccatgccgaggccactgcgaacggccacgggcgaggccactgc
                                                                                                                                                                                                                                183 TGGCGCCGGCGCACAGG---TGGCGCGGCGGCGCGGCGGGGGCCGGGGGGCGGG
                                                                                                                                                                                                                                                                                315 gaacggcaagaccaacggccaccgcgagagcaacggccatgctgaggccgccgacgcgaa
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TD 193610 standard; DNA; 3946
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This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunishing against M. tuberculosis infection or may be used for the diagnosis of tuberculosis.
gaacggcaagagcaacggccatgccgaggccactgcgaacggccacggcgaggccactgc 314
                                                                                                  374
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                                                                                          315 gaacggcaagaccaacggccaccgcgagagagcaacggccatgctgaggccgccgacgaa
                                                                                                                                                                                                                                             300 cGGCCGCGGCGTGACGCGGCGATGGGGCCCAGCGGTCTCGGCCTGGGCCTCTCCGGCTT
                                          240 TACCGGCGCACCGGCGCGTTGTCGCGCCACCGGTAGTGCAGGCATCGGCGGGGCCGG
                                                                                                                                                                                           375 cggcgagagcaacgagcatgccgaggactccgcggggaacggcgagggaac----g
                                                                                                                                                                                                                                                                                                                                                                                                   488 aggacggcgtgctggcggcgacgggggcgaacatgagcatccggggcgatacggtacaaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      608 cgtccgtgttcccggccttccgcacggccgtcgaggccgaggacgccgtcgccgccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 ACGGCGCAACGCGGCGTCGGCCTGACAGCCAAGGCCGGCGACGCGGGGGCGCGCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. tuberculosis immunogenic polypeptide XP25 3'-end DNA. Tuberculosis; immunogenic; soluble; antigen; protective immunity; vaccine; pharmaceutical; infection; diagnosis; ss. Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                428 ggcatgcggcggcggcagaggaggaggaggaggcggtggagtggaatttcgcggggtgcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480 AGGICTCGGCGACAACGGCGGGGTCGGCGGTGACGGTGGGGCCCGGTGGCGC-CGCCGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               668 tgcgcaccggccagttcaactgctaccccgccggcgtcggc 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599 ATGCCGCCAACGGGGGGCGCCGGCGGTGCTGGCGGGGCCGGC 639
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48.7%; Pred. No. 8.9e-07;
Live 0; Mismatches 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 G;
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07-0CT-1997; U18293.
11-0CR-1997; US-8118112.
11-0CR-1996; US-730510.
(CORI-) CORIXA CORP.
Campos-Neto A, Dillon DC, Houghton R, Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS; WPI: 98-261042/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 C;
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Best Local Similarity 48.75
Watches 312; Conservative
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RESULT V64548

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Streptomyces viridosporus dhpA gene.
Streptomyces viridosporus dhpA 4-substituted-1,4-dihydropyridine;
symmetric hydrolase; dhpA, 4-substituted-1,4-dihydropyridine;
derivative; Streptomyces viridosporus; ester; chiral; synthesis;
cardiovascular; treatment; hypertension; ischaemic heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                     cgaacggcaagagcaacggccatggcgtggctgccgccgtgaacggcaagagcaacggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3344 TGTTCGCCACCGGCGCGCGCGTCGGCGGATCCGGTGGGGCCCGCCAGCTCCGGCGGGGGCCGGTG
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DNA sequences can be used for diagnosing tuberculosis and other mycobacterial infections in humans or animals, for identifying mycobacteria in (clinical) samples by hybridisation or amplification, including differentiation between strains, as well as for epidemiological studies, for monitoring vaccination or for the development of anti-mycobacterial drugs and vaccines. Sequence 3946 BP; 518 A; 1541 C; 1345 G; 542 T;
                                                                                                                                                                                                                                                                                                                                 tggccaccgtacgccagagggagtcgccgcgaacggccttgccgtggccgcagccg
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Έ
                                                                                                                                                                                                                              Length 3946;
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                                                                                                                                                                                                                              Score 77.8; DB 1;
Pred. No. 3.1e-06;
); Mismatches 342;
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Best Local Similarity
Matches 318; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       Asymmetric hydrolase gene derived from Streptomyces viridosporus acts on 4-substituted-1,4-di:hydro:pyridine derivatives to produce chiral derivatives useful for synthesis of cardiovascular drugs Claim 3; Page 49-55; 78pp; Japanese.

This sequence is the Streptomyces viridosporus dhpA gene which encodes an asymmetric hydrolase which acts on 4-substituted-1,4-dihydropyridine esters to chiral partially hydrolysed derivatives. The enzyme allows the efficient conversion of 4-substituted-1,4-dihydropyridine esters to chiral partially hydrolysed derivatives, for use in the synthesis of cardiovascular drugs suitable for the treatment of e.g. hypertension and ischaemic heart disease. Sequence 2539 BP; 433 A; 959 C; 867 G; 280 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1816 CAAGGCGCTCCAGCAGACCGTGATCGCCGACCCGGTCTCGGTGAGCTTCGGCGTCCAGCA 1875
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Pred. No. 8.1e-06;
0; Mismatches 561; Indels
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31-JUL-1995; JP-212975.
29-FEB-1996; JP-067478.
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Arisawa A, Dobashi K,
Tsuruta T, Yoshioka T;
WPI; 97-145682/13.
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This sequence is a fusion gene encoding Streptomyces viridosporus dhph gene product (an asymmetric hydrolase) which acts on 4-substituted-1,4-dihydropyridine derivatives, and melanin from S. antibioticus. The Dhpa enzyme allows the efficient conversion of 4-substituted-1,4-dihydropyridine esters to chiral partially hydrolysed derivatives, or addiovascular drugs suitable for the treatment of e.g. hypertension and ischaemic heart disease. sequence 2809 BP; 473 M; 1041 C; 984 G; 311 T;
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737
 ccagitcaacigctaccccgccggcgtcggcctccccgccgcacgaagcgccgiggcaga
                    2056 CGTCGACATGACCGCCGACACCCGGCTCGGCGGCACGGTGGACGGCGCGTACTCGGCGTA
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31-JUL-11995; JP-212975.
29-FEB-1996; JP-067478.
(SAOC ) MERCIAN CORP.
Arisawa A, Dobashi K, I
TSULUTA T, YOSHIOKA T;
WPI; 97-145682/13.
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Score 75.4; DB 1;
Pred. No. 8.2e-06;
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                                      Best Local Similarity
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Disclosure; Page 23-24; 32pp; English.

Disclosure; Page 23-24; 32pp; English.

This polynucleotide comprises a synthetic RNA sequence coding for the plo5 subunit (see W46593) of human telomerase and optimised for expression in mammalian cells. It is based on an isolated cDNA clone (see V03369) for plo5.

The invention provides methods relating to human telomerase and related nucleic acids, including the subunit proteins pl40, pl05, pl8 and p43. The proteins may be produced recombinantly from transformed host cells or purified from human cells. Also included are human telomerase RNA (see V05373) and functional derivatives (see V05374 and V16092-93), as well as pl05 synthetic DNA sequences (V05370-72). The invention also provides isolated telomerase hybridisation probes and primers capable of specific binding agents such as specific antibodies, and methods of maxing and using the subject compositions in diagnosis (e.g. maxing and using the subject compositions in diagnosis (e.g. maxing and using the subject compositions in diagnosis (e.g. genetic hybridisation screens for telomerase gene expression) and in the blopharmaceutical industry (e.g. reagents for screening chemical libraries for lead agents). Modulation of telomerase centernance of cancer, and analysis of the prevention of cancer, and an execution of cancer.
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New nucleic acid encoding human telomerase proteins or their fragments - useful for therapeutic modulation of telomerase activity and for screening for potential modulators of telomerase-target
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                                                                                      06-JUL-1998 (first entry)

Human telomerase pl05 subunit mammalian optimised synthetic RNA.

Telomerase; pl05; human; cell replication; cancer; restencsis;
multiple sclerosis; inflammation; rheumatoid arthritis;
myocardial infarction; glomerulonephritis; transplant rejection;
infection; therapy; ds.
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45.8%; Pred. No. 1.3e-05;
Live 0; Mismatches 388; Indels 6,
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                                             standard; RNA; 2277
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Matches 333; Conservative
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08-JUL-1996; US-676974.
(REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                     15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                              Collins K;
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                                             V05372
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RESULT
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                                                                                                                                                                                                             1005 GACCGTGTTCATCCGCAACCTGAGCTTCGACAGCGAGGAGGAGGAGCTGGGCGAGCTGCT 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACCTGGCCGTGACCCGCGACGAGGCCGCCAAGCTGCAGACCAAGGTGAAGAAGC 1301
                                                                                                                         945 GGCCGTGCAGGTGAGCAACAAGAAGCGCCAAGCTGCCCAGCGACGTGAACGAGGGCAA 1004
                                                                                                                                                                                                                                                                                                 1065 GCAGCAGTTCGGCGAGCTGAAGTACGTGCGCATCGTGCTGCACCCCGACACCGAGCACAG 1124
                                                                                                                                                                                                                                                                                                                                                                                    1125 CAAGGGCTGCGCCTTCGCCCAGTTCAT---GACCCAGAGGCCGCCCAGAAGTGCCTGCT 1181
372 gaacggcgagagcaacgagcatgccgaggactccgcgggcgaacggcgaggagcaacgggca 431
                                      885 CATCGACGACGAGGAGGTGGCCCCAGAGCGACACCAGCACCGAGGAGCAGGAGGACAA 944
                                                                                                                                                                                                                                                          cgcgagcgtgcaggagaaggggccgcgggcccgtgccgctggcccacgggggacccgtc 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggcagagcacctgtcgcagggcgtgccgtacatgctatcggccgacgacgtcttcctcac 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens mammalian codon-optimized telomerase protein p105 gene. telomerase; p105; treatment; prevention; cancer; restenosis; inflammation; myocardial infarction; glomerulonephritis; transplant; rejection; infection; HIV; human immunodeficiency virus; bone marrow transplants; proliferation-restricted cells; codon-optimized; mammalian cell expression; ds.
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The sequence is that of a human telomerase protein coding sequence codon-optimized for mammalian cell expression. The sequence, or specific fragments of it, can be used to modulate expression of a telomerase transcript (by hybridising to it intracellularly), e.g. for treatment or prevention of cancer, restenosis, inflammation, myocardial infarction, glomerulonephritis, transplant rejection and infections (e.g. with human immunodeficiency virus). It can be used express recombinant telomerase protein which can be used to screen for agents, e.g. antibodies, that modulate binding of human telomeras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding human telomerase protein p105 or its fragments - used for therapeutic modulation of telomerase activity and for screening for potential modulators of telomerase-target
                                                                                   tgcggcggcggcggcagaggaggaggaggcggtggagtggaatttcgcggggtgccaagga
                                                                                                                                                                    492 cggcgtgctggcggcgacgggggggggaacatgagcatccggggcgatacggtacaagatcag
                                                                                                                                                                                                                                                                                                                                                cgtgttcccggccttccgcacggccgtcgaggccgaggacgccgtcgccgccgtcgtgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                 672 caccygccagttcaactgctaccccgccggcgtcggcctccccgccgcacgaagcgccgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1182 GGCCGCCAGCCCCGAGAACGAGGCCGGCCGGAGCTGGACGGCCGCCAGCTGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V13836 standard; cDNA; 2277 BP.
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08-JUL-1996; US-676967.
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to its binding target. Those that inhibit telomerase activity can be used to treat the conditions listed above, while those that are agonists can be used to treat the conditions listed above, while those that are calls, especially normal somatic cells, e.g. in cases of hypersensitivity or atrophy, also to improve production of recombinant proteins by maximising cell density and survival and expansion of precursor cells being used for bone marrow transplants. They may also be used for diagnosis. Other uses of telomerase proteins are isolation, enrichment and concentration of telomerase proteins proteins; as immunogens; in therapy; as reagent where nascent oligonucleotides of known structure are needed (e.g. for tagging the native nucleic acid molecules) and for regulating cell growth/density collerance. The agents and the telomerase proteins should be very specific, e.g. they are selective for cancer cells without harming
                                                                                                                                                                                                                                                                                                                                                                                                                        216 T;
                                                                                                                                                                                                                                                                                                                                                                                                                        781 G;
                                                                                                                                                                                                                                                                                                                                                                                                                        723 C;
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X53491/C TD X53491 standard; DNA; 114955 BP.

ñ 125 caadgecrececrirececeaerrear -- dacecadadececeagaagreceret 1181 1005 GACCGIGITCAICCGCAACCIGAGCIICGACAGCGAGGAGGAGGAGCIGGGCGAGCIGCI 1064 945 GGCCGTGCAGGTGAGCAACAAGAAGAAGCGCAAGCTGCCCAGCGACGTGAACGAGGGCAA 1004 .065 GCAGCAGTTCGGCGAGCTGAAGTACGTGCGCATCGTGCTGCACCCCGACACCGAGCACAG 1124 551 731 195 ccatggcgtggatgccgacgcgaacggcaagagcaacggccatggcgtggctgccgacgc 254 824 431 491 75 catggccaccgtacgccagagcgacggagtcgccgcgaacggccttgccgtggccgcagc 134 644 135 cgcgaacggcaagagcaacggccatggcgtggctgccgccgtgaacggcaagagcaacgg 194 645 GGAGAGCGTGAAGAAGAAGGCCCGCGAGGAGGAGGACATGGAGGAGGAGGAGGACGACGA 704 705 CGACGACGACGACGACGAGGAGGACGCGTGTTCGACGACGAGGACGAGGAGGAGGA 764 255 gaacggcaagagcaacgg···ccatgccgaggccactgcgaacggccacggcgaggccac 311 312 tgcgaacggcaagaccaacggccaccgcgagagcaacggccatgctgaggccgccgacgc 371 Gaps 585 CAAGGACACCCAGAGCGTGAGCGCCATCGGCGAGGAGAAGAGCCACGAGGAAGCAACCA 492 cggcgtgctggcggcgacggggggggaacatgagcatccgggcgatacggtacaagatcag 672 caccggccagttcaactgctaccccgccggcgtcggcctccccgccgccgcacgaagcgccgt 765 GAACATCGAGAGCAAGGTGACCAAGCCCGTGCAGATCCAGAAGCGCGCGTGAAGCGCCC 372 gaacggcgagagcaacgagcatgccgaggactccgcgggcgaacggcgaggaacgggca 432 tgcggcggcggcggcagaggaggaggaggcggtggagtggaatttcgcggggtgccaagga 552 cgcgagcgtgcaggagaagggccgcggcccgtgctgccgctggcccacggggacccgtc 885 CATCGACGACGAGGAGCTGGCCCAGAGCGACACCAGCACGAGGAGCAGGACAA cgtgttcccgggccttccgcacggccgtcgaggccgaggacgccgtcgccgccgtgcg ; 6 Length 2277; 0; Mismatches 388; Indels DB 1; Score 74.2; Pred. No. 1. 3.9%; Query Match
Best Local Similarity 45.89
Matches 333; Conservative 612 g 엄 ద 음 à à ò à 셤 ò g ò g δ 셤 ö 엄 οy g ò

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Vascociaristriction

Vascociaristriction

Vascociaristriction

C directed against at least 2 marks selected from target genes, coding and

C directed against at least 2 marks selected from target genes, coding and

C directed against at least 2 marks selected from target genes, coding and

C initiation codons, genomic flanking regions, intron exon borders, the

C f'end, the 3'-end and the juxta-section between coding and non-coding

C regions and all segments of RNAs encoding proteins associated with one

CC more diseases, conditions or mixtures. The antisense oligonucleotides

CC may be derived from sequences X5572-74. These multiple target

CC oligonucleotides (specifically X55180-271) can be used for the antisense

CC coligonucleotides (specifically X55180-271) can be used for the antisense

CC treatment of diseases and conditions. Typical diseases and conditions

CC treatment of diseases and conditions. Typical diseases and conditions

CC treatment of diseases, pulmonary vasoconstriction, inflammation,

CALLENGE ASSOCIATED AND ASSOCIATED ASSOCIATED AND ASSOCIATED AN
                                                OS-JUL-1999 (first entry)

Human adenosine Al receptor antisense oligonucleotide fragment.

Human adenosine Al receptor antisense oligonucleotide fragment.

Antisense oligonucleotide; multiple target; antisense treatment;

impaired respiration; inflammation; lung disease;

pulmonary vasoconstriction; inflammation; allergic rhinitis;

acute asthma, allergy; asthma; impeded respiration;

respiratory distress syndrome; pain; cystic fibrosis;

pulmonary hypertension; pulmonary vasoconstriction; emphysema;

chronic obstructive pulmonary disease; leukemis; lymphoma; carcinoma;

colon cancer; breast cancer; lung cancer; pencreatic cancer;

hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1998; U19419.
09-JUN-1998; US-093972.
17-SEP-1997; US-059160.
(UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate cancer; ss.
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Db 104880 GGGNNHNNNSVGGCCVGCGGNNHNNNSCVGGCCVGCGGNNHNNNSCCVGGCCVGCGGNNH 104821 Db 104700 CCVGGCCVGCGGNNHNNNSGGCGCGCCCVGGCCVGCGGNNHNNNSCGGCGCGCCCVGGCC 104641 104820 NNNSCCCVGGCCVGCGGNNHNNNSGCCCVGGCCVGCGGNNHNNNSCGCCCVGGCCVGCGG 104761 104760 NNHNNNSGCGCCCVGGCCVGCGGNNHNNNSCGCGCCCVGGCCVGCGGNNHNNNSGCGCGC 104701 cgtttcctcatggccaccgtacgccagagcgacggagtcgccgcgaacggccttgccgtg 126 gocgacgcgaacggcaagagcaacggccatgccgaggccactgcgaacggccacggcgag 306 127 gccgcagccgcgaacggcaagagcaacggccatggcgtggctgccgccgtgaacggcaag agcaacggccatggcgtggatgccgacgcgaacggcaagagcaacggccatggcgtggct ώ, Length 114955; Indels 3.8%; Score 73; DB 1; Les 30.8%; Pred. No. 4.2e-05; ive 97; Mismatches 494; Query Match 3.8%; Best Local Similarity 30.8%; Matches 264; Conservative 67 187 247 엄 a δ δ

1241

242 GGACCTGGCCGTGACCCGCGACGAGGCCGCCAAGCTGCAGACCACCAAGGTGAAGAAGCC 1301

ggcagagcacctgtcgcagggcgtgccgtacatgctatcggccgacgtcttcctcac

GGCCGCCAGCCCCGAGAACGAGGCCGGCGGCCTGAAGCTGGACGGCCGCCAGCTGAAGGT

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Db 104100 GACGCCGNNHNNNSGCCCGGCCCGACGCCGCNNHNNNSGCCCGGCCCGACGCCGCCNHN 104041
                                                                             Db 104640 vGCGGNNHNNNSGCGGCGCGCCCVGGCCVGCGGNNHNNNSGGCGGCGCGCCCVGGCCVGC 104581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 104400 CGCGCCCVGGCCGNNHNNNSCCCGGCCGCCGCGCGCCCVGGCCVGCGGNNHNNNS 104341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 104340 GCCCGGCCGGCGCGCCCCVGCCCVGCGGNNHNNNSGGCCCGGCGGCGCGCGCCCVG 104281
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                                                                                                                                                                                                                                                                                                                                                                                                               Db 104520 CGGNNHNNNSGCCGGCGCGCGCCCVGCCVGCGGNNHNNNSGCCGGCGCGCGCCCCVG 104461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 104460 GCCYGCGGNNHNNNSCGGCCGGCGGCGCCCCYGGCCCYGCGGNNHNNNSCCGGCCGGCG 104401
                                                                                                                                                                                                                                        GENNHNNNSCEGEGEGEGECCVEGECVECEGENNHNNNSCEGEGEGEGECECCVEGECVE 104521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             843
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gocactgogaacggcaagaccaacggccaccgcgagagcaacggccatgctgaggccgcc 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 37; 120pp; English
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US-059160
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17-SEP-1998; U19419.
09-JUN-1998; US-0939
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directed against at least 2 mRNAs selected from target genes, Coding and non-coding regions of RNAs corresponding to target genes, coding and non-coding regions of RNAs corresponding to target genes, coding and non-coding regions, genomic flanking regions, intron-exon borders, the firstion codons, genomic flanking regions, intron-exon borders, the common diseases, conditions or mixtures. The antisens oligonucleotides or may be derived from sequences X55272-74. These multiple target colligonucleotides (specifically X5518-774) can be used for the antisense colligonucleotides (specifically X5518-774). Takes multiple target tractment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, callergic rhinitis, acute asthma, allergies, asthma, impeded respiration, callergic rhinitis, acute asthma, allergies, asthma, impeded respiration, callergies, actions of disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, hepatice metastases, as well as all types of cancer, metanoma, hepatic metastases, as well as all types of cancer, metanoma, metastases, cancer, lungs, including breast and prostate cancer.

Sequence 114955 BP; 6071 A; 29417 C; 35712 G; 21328 T;
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Similarity 35.0%; Pred. No. 0.00018;
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18-ARP-1997:

29-ARP-1997:

29-ARP-1996: DE-017184.

(GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.

18 Eppida C, Honisch C, Moreno C, Singh M;

WPI: 97-549750/50.

19 P-SDB; W31852-55.

19 P-SDB; W31852-55.

19 P-SDB; W31852-55.

19 P-SDB; W31852-55.

10 P-SDB; W31852-55.

10 P-SDB; W31852-55.

10 New DIMA and related proteins or RNA derived from M. tuberculosis related proteins of anti-mycobacterial agents.

10 New claimed DNA (A) has one of 3 isolated Mycobacterium cuberculosis DNA sequences of 3946 bp (1) (T93610), 2653 bp (VI)

10 New claimed DNA (A) has one of 3 isolated Mycobacterium cuberculosis DNA sequences of 3946 bp (1) (T93610), 2653 bp (VI)

10 New claimed DNA (A) has one of 3 isolated Mycobacterium cuberculosis DNA was screened With degenerate probes of 39511) or 440 bp (IX) (see T93612), or hybridises to, or is a confident of the conceled part of (A), and proteins encoded by (A). To isolate (I), a cosmid of (A), and proteins concaled by (A). To isolate (I), a cosmid of (A), and proteins (See W31852-55). These ORFs can be amplified and concelled into vectors for expression in E. coll or other mycobacterial infections in humans or animals, for identifying mycobacterial infections in humans or animals, for identifying mycobacterial in (clinical) samples by hybridisation or mycobacterial in (clinical) samples by hybridisation or for mycobacterial in molitoring vaccination or for the development of antimycobacterial drugs and vaccination or for the development of antimycobacterial drugs and vaccination or for the development of antimycobacterial drugs and vaccines.

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Pred. No. 0.00011;
); Mismatches 361; Indels 3
                                                                                                                                                             Mycobacterium tuberculosis genomic DNA fragment (I). Tuberculosis; mycobacteria; infection; diagnosis; antimycobacterial; antibiotic; vaccine; ss. Mycobacterium tuberculosis.
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T93610
ID T93610 standard; DNA; 3946 BP.
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Best Local Similarity 45.9°
Matches 309; Conservative
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DNA procedure Streptomyces ambofaciens platenolide synthase domain - The strength will be a production of spiramycin-related polyketide antibiotics

Tor production of spiramycin-related polyketide antibiotics

Claim 9: Pages 8-33; 81pp; English.

Claim 9: Pages 8-33; 81pp; English.

Control This sequence represents the platenolide street of as the srmG gene, and was invention. This sequence is referred to as the srmG gene, and was invention. This sequence encodes the culti-functional proteins which direct the synthesis of the polyketide platenolide. Platenolide is the basic building block of the macrolide antibiotic spiramycin. The DNA can be used to produce compounds and derivatives. Modifications of the platenolide synthase DNA sequence can be made so as to change the number and type of carboxylic acids incorporated into the growing polyketide chain and to change the kind of post-condensation processing that is conducted.

Sequence 44377 BP; 4965 A; 15552 C; 17381 G; 6479 T;
                                                                                                                                                                        CAGGCCGGCGTTGCCGGCAGCCCCGCCGGCCCGGCCCCGCGCGTGAGGGCTACTAC 3495
                                                                                                                                                                                                                                           geogeogeogtgogeacoggecagtteaactgotacceogeoggogtcggceteccegec 717
                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1998 (first entry)
Platenolide synthase gene cluster.
Platenolide synthase gene cluster; platenolide production; srmG gene; multi-functional protein; macrolide antibiotic; spiramycin; ss.
                                                                                                      gggtgccaaggacggcgtgctggcggcgacgggggcgaacatgagcatccgggcgatacg
                                                                      gtacaagatcagcgcgagcgtgcaggagaaggggccgcgggcccgtgctgccgctggccca
                                                                                                                                            cggggacccgt--ccgtgttcccggccttccgcacggccgtcgaggccgaggacgccgtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ORF4 encodes protein shown in W23719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "ORF2 encodes protein shown in W23717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuhstoss SA, Rao RN, Richardson MA;
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/note= "ORF2 e:
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Burgett SG, Kuhstoss SA
Rosteck WPI; 97-418047/39.
P-PSDB; W23716-W23720.
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        Length 44377;
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Score 67.4; DB 1;
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Best Local Similarity 45.7%;
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T41757 10338 Lambd
A1116859 ue29d01.9
A394723 26506 Lam
A1048570 ud61e01.9
C91185 C91185 Dict
A1447927 E872246249
A1562691 TENS2678
A1562691 TENS2678
A156369 v988503.r1
W43288 22681 Lambd
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A1001356 Mrsr6-A6.
AA650709 30823 Lambd
AA650709 30823 Lam
AB009149 AB009149
C72041 c72041 Rice
A137786 gqv13002.x
A1389106 GH20192.5
A1063350 CH03102.3
A1659767 t994f08.x
A169972 tff8a03.x
A169972 tff8a03.x
A1658863 tt98f04.x
A165888 co07405.x
A1195517 qe61c01.x
A1453638 tj45910.x
A1453638 tj45910.x
A1654026 wd13h09.x
                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                   Description
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AI619119
D251821
D251821
AU056779
238084
T13684
D23043
AA980369
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AA194757
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AI453638
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AI001336
AA650709
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AI184898
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em_est23:*
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Zea

DEFINITION ACCESSION

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RESULT A1657244 LOCUS

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Poaceae; Zea
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Matches 399;
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DEFINITION
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                             /organism="Zea mays"
/cultivar="B73" .
/db_xref="taxon:4577"
/clone_lib="486 - leaf primordia cDNA library from Hake
                                                                                                                                                                                                                                                                                                                                           CDNA
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Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                             University
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189324.
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                                                                                                                                                                                                                                                                                                                                           zab;
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                                                                                                                                                                                                                                                                                                         /tissue_type="leaf primordia"
/dev_stage="p7-p1] leaf"
/lab_host="E.coli XL1-Blue MFR'"
/note="Organ: shoot; Vector: Lambda
                                                                                                                                                                            USA
                                                                                                                                        Contact: Walbot V
Department of Biological Sciences
Standord University
Staniord University
Tel: 650 723 2227
Fax: 650 728 8221
Fax: 650 728 8221
Fax: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Score 372.6; DB 49;
Pred. No. 1e-53;
0; Mismatches 109;
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Best Local Similarity 80.3%;
Matches 462; Conservative
                                                              (bases 1 to 571)
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198 c
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                     Zea mays
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          Zea
                     ORGANISM
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ORIGIN
                                                              REFERENCE
AUTHORS
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KEYWORDS
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                                                                                                                                                                                                      EST 21-APR-1999
CDNA library from Hake lab Zea
1021 cocaacaacccgtgcggcagcgtttactcctacgaccatctgtccaaggtcgcggaggtg 1080
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                      Unpublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948200.
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/dev_stage="P7-P11 leaf"
/lab_host="E.coli XL1-Blue MFR'"
                                                                      1081 gcgaaaaggctcggaatattggtgattgctgacga 1115
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primordia
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                                                                                               Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

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486073F11.x2 486 - leaf p
mays cDNA, mRNA sequence.
AI619119
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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RICS14756A Rice green shoot Oryza sativa cDNA, mRNA sequence.
D48521
                                                 tttgettgtgttccatettetettcaagatggteteggaaggateaaateattetgteaa
                                                                                                                                                                                                                           113 CCCACTTCCATCGTTTTCCCCTGTATCATCAACAAAAGTGTAACATTGAAATCCCTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Tice Genome Research Program
2-1-2 Kannondal, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
86 c 105 g 132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 0298-38-7468
Fax: 0298-38-7468
Email: tsasak/@abr.affrc.go.jp
Insert Length: 852 Std Error: 0.00
High quality sequence stop: 405.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 459)
Sasaki,T., Miyao,A. and Yamamoto,K.
Rice cDNA from callus 1995
Unpublished (1995)
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D48521.1 GI:702230
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Tel: 0298-38-7441
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TITLE
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COMMENT
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ORIGIN
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnoliophyta, Liliopsida, Poales,
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                                                                                                                                                                                                                                                                                                                                                                                    1316 atgicingacagacccagcaaccticaticaggcagcicticcicagaitcitigagaaca 1375
                                                                                                                                                                                                                              1196 tagggtetetgteeaagteatggatagtgeetggatggeggettggatgggtageggtgt 1255
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RICR3343A Rice root Oryza sativa cDNA clone R, mRNA sequence.
D25143
9428987
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                                                                        taaaccccaacaacccgtgcggcagcgtttactcctacgaccatctgtccaaggtcgcgg
                                    61 TAMATCCCAATAATCCATGCGGGAATGTGTACACTTACGAGCATTTATCCAAGGTGGCAG
                                                                                                                                                     tgggcagcgccccgttcatcccaatgggagtgtttgggcacatcacccctgtgctgtcca
                                                                                                                                                                                                                                                                                                           1256 acgaccccagaaagatcttacaggaaactaagatctctacatcaattacgaattacctca
                                                                                                                                                                                                                                                                                                                               ä
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Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
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/note="Prepared from seedling root.
69 c 97 g 119 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1376 caaaggaagatttctttaaggcgattattggtctgctaaag 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 0298-38-7441
Fax: 0298-38-7468
Email: minobe@rtcs0.riken.go.jp
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Location/Qualifiers
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1 (bases 1 to 410)
Minobe,Y. and Sasaki,T.
Rice cDNA from root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yuzo Minobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:428987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
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Oryza sativa
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Oryza sativa.
Oryza sativa
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Oryza.
                                                                     1191
                                                                                                                                       1192 tecatagggtetetgteeaagteatggatagtgeetggatggeggettggatgggtageg 1251
                                                                                                                                                                                                       1252 gigiacgacccagaaagaictiacaggaaactaagaictiacaatcaattacgaattac 1311
                                                                                                                                                                                                                                                                          1312 ctcaatgtctcgacagacccagcaaccttcattcaggcagctcttcctcagattcttgag 1371
                                                                                                                                                                                                                                                                                                                                          1372 aacacaaaggaagatttetttaaggegattattggtetge-taaaggaateateagagat 1430
                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU056779 464 bp mRNA EST 29-APR-1999 AU056779 Oryza sativa mature leaf Nipponbare Oryza sativa CDNA clone S20870_1A, mRNA sequence.
                                                                                     62 GITTITIGGGAGITCCCCATITGTCCCAAFGGGITGCITTGGGCACATCGIACCAATAIA 121
                                                                                                                                                         gttctgggcagcgccccgttcatcccaatgggagtgtttggggcacatcaccctgtgctg
                                                                                                                                                                                                                                                                                                                                                                              302 AATACCAAGGAAGAATTCTTTAAGAGGATAATTGATTTGCTTACGGGAAACATCAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leaf Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                          1 others
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Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
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/db_xref="taxon:4530"
/map="11q"
/clone="$20870_1A"
/clone=lib="cryza sativa mature le
/tissue_type="mature leaf"
a 109 c 105 g 132 t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, K. and Sasaki, T.
Rice cDNA from mature leaf
Unpublished (1999)
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-1994
CDNA clone VBVMA10 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H., Rouze P., Caboche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Versailles-VB"
/note="Vector: pBluescript; tissue=whole seedlings of A
/note="vector: pBluescript; clone_library=Versailles-VB;
cloning vector: pBluescript (Stratagene); Physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1046
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                                                                                                                                                                                                                                                                                                                                     237
                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                                                                     61 CTGTGATCTTCCTTACAAGCTTTGCACAGATGATATTTTCCTCACATCTGGAGGTACCCA 120
                                      Gaps
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                                                                                                                                                                                                                                             121 AGCAATCGAGATTGTTATGTCTGTTTTTGGCCA---ACCAGGTGCCAATATATTGCTTCC
                                                                                                                                                                                                                                                                                                                    178 AAAGCCCGGGTACCCAAAACATGAAGCACATGCGGTGTTCCACAGGATGGAAGTGCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 AGATGAGAATACTGTTGCAATAGTGATTACTAACCCCAATAACCCTTGTGGGTAATGTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctgctaccccgccggcgtcggcctccccgccgcacgaagcgccgtggcagagcacctgtc
                                                                                                           747 gcagggcgtgccgtacatgctatcggccgacgacgtcttcctcaccgccggcgggaccca
                                                                                                                                                                                                                                                                                                   caggccaggctacccaaactacgaggcgcgcgcgcgttcaacaggctggaggtccggca
                                                                                                                                                                                                                                                                                                                                                                                                           238 CTATGATCTTGTTCCAGAGAGGATGGGAGATTAATGTTGAAGCTGTTGAAGCTTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgacaagaacaccaccgccatggtcatcataaaccccaacaaccgtgcggcagcgttta
                                                                                                                                                                                                                           ggcgatcgaggtcataatcccggtgctggcccagaccgccggcgaccaacattctgctccc
                                    3;
 Length 464;
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                                      Indels
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ATTS4224 Versailles-VB Arabidopsis thaliana
mRNA sequence.
 49;
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                                      167;

    .446
    /organism="Arabidopsis thaliana"

Score 182.4; DB 4
Pred. No. 8.1e-22;
0; Mismatches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratoire de Biologie Cellulaire
Route de Saint-Cyr, 78026 Versailles
Email: Literry@versailles.inra.fr.
Location/Qualifiers
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/db_xref="taxon:3702"
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 9.5%;
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Arabidopsis thaliana
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                                      Conservative
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                   Similarity
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                                  Matches 295;
 Query Match
Best Local 3
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ORGANISM
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/dyntam." Arabidopsis chartaua
/db_xref="taxon:3702"
/db_xref="taxon:3702"
/db_xref="taxon:3702"
/clone="149B197"
/clone="149
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIncbsh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        969 ctcgctggaatccatcgccgacaagaacaccaccgccatggtcatcataaaccccaacaa 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1029 cccgtgcggcagcgtttactcctacgaccatctgtccaaggtcgcggaggtggcgaaag 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 IGGICTCGAGGITCGCAAGITINAICTICTTCCGAGAAAGAATGGGGAGATTGATCTINA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r 07-JAN-1998
clone 35D4T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               849 egecaacattetgeteeceaggecaggetaeceaaactaegaggegegegegteaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          909 caggctggaggtccggcatttcgacctcatccccgacaaggggtgggagatcgacatcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 AGGTATCGAAGCCATTGCAGACGAGAAAACTGTGGCTATGGTTGTAATTAACCCCAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 ICCCIGIGGAAAIGICTACICICACGACCAICICAAAAAGGIIGCAGAGGCIAGGAA
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1849 Lambda-PRL2 Arabidopsis thaliana cDNA (
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Pred. No. 2.3e-13;
0; Mismatches 89;
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                                                                                                                                                                                              /organism="Arabidopsis
                            Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.9%;
Best Local Similarity 67.3%;
Matches 183; Conservative C
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1 (bases 1 to 470)
Newman,T., deBruih,F.J., Green,P., Keegstra,K., Kende,H.,
Newman,T., ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
Plant Physiol. 106, 1241-1255 (1994)
On Apr 14, 1993 this sequence version replaced gi:693132.
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11148 Lambda-PRL2 Arabidopsis thaliana cDNA clone 149B19T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                        973 ctggaatccatcgccgacaagaacaccaccgccatg-gtcatcataaaccccaacaacc 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GTCGAGGCTCTTGCAGACAAAACACGGTTGCTTTTANTTGTNATAAACCCTGGTAATCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 CITTAAAGGACCCTAAGAICATIGAGAGGITTAAGAAATACTITGATATICTIGGIGGAC 420
                                                                                                                                                                                                                                                                                                                             Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PEL, Michigan State University, Plant Biology Bldg.,E.
Lansing,Mi
                                                                                                                                                                                           Length 446;
                                                                                8 others
                                                                                                                                                                                     7.9%; Score 151.6; DB 20; Length ilarity 61.0%; Pred. No. 1.2e-16; Conservative 0; Mismatches 172; Indels
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conditions: in vitro-grown old."
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/clone="135D417"
/clone="11b="Lambda-PRL2"
/clone_lib="Lambda-PRL2"
/clone_lib="Lambda-PRL2"
/octe="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA. "
13 others
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Oryza sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnoliophyta, Liliopsida, Poales,
Poaceae, Oryza,
1 (bases 1 to 343)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D23043 343 bp mRNA EST 20-JUL-1998
RICC2086A Rice callus Oryza sativa cDNA clone R, mRNA sequence.
D23043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GGTTTCTTGTGATTNCTGATGAGGTTTACGGTCATCTTTGCTTTTGGTAGCAACCGTTTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 INCCAATNGGIGIGITITGGATCTATIGINCCIGIGCTIACTCTIGGNICITIAICAAAGA 241
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                                                          Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, Mi
Tel: 517-533-0884
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TCGAGGCTCTTGCAGAGGAAAACACGGTTGCTTTGGTTGTTATAAACCCNGGTAATCCTT
  95148729
On Nov 29, 1993 this sequence version replaced gi:430053
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tive 0; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                        /strain="var columbia"
                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3702"
/map="4"
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Matches 175; Conservative
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// ...343
/organism="Oryza sativa"
/strain="cultivar Nipponbare, sub_species Japonica"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="R"
/clo
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1123 ggcaagctggttctgggcagcgcccgttcatcccaatgggagtgtttgggcacatcacc 1182
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Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                  National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
PROJECT = 'KCP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                   Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:4630651
Rice cDNA from callus
Unpublished (1994)
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481 ATCCATGATCGAAGAGACATTTT 503
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Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Mammalia;
Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

[ (Dasss 1 to 719)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA980369 719 bp mRNA EST 27-MAY-1998 ua52c12.rl Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1350358 5' similar to gb:X5250_cds1 TYROSINE AMINOTRANSFERASE (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                     CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttgcttgtgttccatcttctcttcaagatggtctcggaaggatcaaatcattctgtcaaa 1696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 GGCATAAGAAGAATITGCTTAATGGCCATTAACTATTCGACTTCAAAGTTGTTAC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/map="12; 4p16.1-4pter"
/clone_lib="486 - leaf primordia cDNA library from lab"
                                                                                                                                                                                                                                                                                                                                /note="Organ: shoot; Vector: Lambda zap; Hake lab
20, 1998 this sequence version replaced gi:2980517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jan 19, 1998 this sequence version replaced gi:2152585.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 108.8; DB 49; Length
Pred. No. 1.7e-09;
0; Mismatches 82; Indels
                                          Department of Biological Sciences Stanford University Stanford University California wave, Palo Alto, CA 94304, US; Tel: 650 723 227
Fax: 650 725 8221
Email: Walbordstanford.edu
Plate: 486092 row: E column: 01.
                                                                                                                                                                                                                                                                                /tissue_type="leaf primordia"
/dev_stage="P7-P11 leaf"
/lab_host="E.coli XL1-Blue MFR'"
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                                                                                                                                                                                      'organism="Zea mays"
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                                                                                                                                                                                                      /cultivar="B73"
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AA980369.1 GI:3158905
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ilarity 65.8%;
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                               Contact: Walbot
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Best Local S
Matches 158
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Park Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Final: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:659150
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 463.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ACATIGGCIGAGTCTAIGGGGAITGAGGICAAGCICTACAAICTAITGCCIGAGAAGICT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772 geogaegaegtetteeteaeegeeggeggaeeeeaggegategaggteataateeeggtg 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 TGGGAAATTGATCTAAAACAACTGGAATCTCTGATCGACGAAAAAACAGCTTGTCTCGTG 241
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                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6 x CBA"
/bb.xref="taxon:10090"
/clone="TtAGE:1350388"
/clone_lib="Stratagene mouse lung 937302"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 2.4e-08;
0; Mismatches 233;
                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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Best Local Similarity 52.9%;
Matches 266; Conservative 0
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GI:557616
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 512)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                           08-JUL-1997
Mus musculus cDNA
TYROSINE
                                                                                                                                                                                                                                                                                                                                                                  Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Fhis clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:535397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             952 tgggagatecgacatcgactcgctggaatccatcgccgacaagaacaccaccgccatggtc 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ACATIGGCTGAGTCTATGGGGATTGAGGTCAAGCTCTACAATCTATIGCCTGAGAAGTCT
                                                                                                                                                                                                                                                                             Waterston,R.
The WashU-HMM Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1398101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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                             AA511748 512 bp mRNA EST v199f11.71 Strategene mouse diaphragm (#937303) clone IMAGE:930477 5' similar to gb:X5520_cds1 AMINOTRANSFERASE (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92.4; DB 34;
Pred. No. 1e-06;
0; Mismatches 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 366. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
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                                                                                                               AA511748.1 GI:2249602
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                                                                                                                                              house mouse.
Mus musculus
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                                                                                        AA511748
                                                                                                   92249602
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Best Local Simi
Matches 249;
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                AA511748
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Arabidopsis.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238047 405 bp mRNA EST 12-OCT-1994
ATTS4207 Versailles-VB Arabidopsis thaliana cDNA clone VBVMA10 3',
mRNA sequence.
238047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="VBVMA10"
/clone_lib="Versailles-VB"
/note="Vector: pBluescript; tissue=whole seedlings of A.
thaliana ecotype Columbia; clone_library=Versailles-VB;
cloning vector: pBluescript (Stratagene); Physiological
conditions: in vitro-grown etiolated seedlings,5 days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Arabidopsis thaliana transcribed genome: the GDR cDNA program Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rouze P., Caboche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1540 gatgacattgattttgctgcaagctcgcaaaagaagaatcagtaatcttatgcccaggg 1599
                                                                                                                                                      goggaggtggogaaaaggotoggaatattggtgattgctgacgaggtatacggcaagctg 1131
                                                                                                                                                                                                                                                             gttctgggcagcgccccgttcatcccaatgggagtgtttgggcacatcacccctgtgctg 1191
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TGGGAAATTGATCTAAAACAACTGGAATCTCTGATCGACGAAAAAAACAGCTTGTCTCGTG
                                                                                                    241 GICAACAACCCGICCAAICCCIGIGGCICIGIGIICAGIAAGCGGCACCIICAGAAGAII
                                                                                                                                                                                                                                                                                                 301 TIGGCAGIGGCIGAAAGGCAAIGCGICCCCAICITAGCCGAIGAGAICIAIGGIGACAIG
                                                                                                                                                                                                                                                                                                                                                                         1192 tecatagggtetetgtecaagteatggatagtgeetggatggeggettggatgg 1245
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Pred. No. 2.7e-06;
0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact.

M., Hofte H.

INRA Versailles
Laboratoire de Biologie Cellulaire
Route de Saint-Cyr,78026 versailles Ce
Email: thierry@versailles.inra.fr.
Location/Qualifiers
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Best Local Similarity 62.0%; Pred. No. 2.7e
Matches 142; Conservative 0; Mismatches
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Seq primer: -40RP from Gibco
High quality sequence stop: 399.
                                                                                                                                                                                                                        A1597379 415 bp mRNA EST 21-APR-1999 Y29fill.y1 Stratagene mouse diaphragm (#937303) Mus musculus CDNA clone IMAGE:930477 5 similar to gb:X52520_cds1 TYROSINE AMINOTRANSFERASE (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 415)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Waterston,R. and Wilson,R., Jackson,Y., Cardenas,M., McCann,R., The WashU-NOT Mouse EST Project 1999
1600 agigitetiggaaiggeaaacigggieegeattaettitgetigitieeatetteteti 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:535397
                               252 ACCGCGTGGGGCTGAACAGAACTGGCTGAGGATAACGTTTGCAGCAGATGCAACTTCGATT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Stratagene mouse diaphragm (#937303)"
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                                                                           4.5%; Score 85.2; DB 48; Length 54.1%; Pred. No. 1.6e-05;
Live 0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .415 // /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="diaphragm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:930477"
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AI597379.1 GI:4606427
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Best Local Similarity 54.1
Matches 196; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     house mouse
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l (bases I to 347)
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
95148729
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bhyta; eudicotyledons; core
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/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1)
day germinated etiolated seedlings; 2) tissue culture
                                                                                                                                                                                       952 tgggagatcgacatcgactcgctggaatccatcgccgacaagaacaccaccgccatggtc 1011
                                                                                                                                                                                                                                                                                   1012 atcataaaccccaacaaccogtgcggcagcgtttactcctacgaccatctgtccaaggtc 1071
                                                                                         1072 goggaggiggcgaaaaggeteggaatatiggigattgetgaegaggiataeggeaagetg 1131
                        241 GTCAACAACCCGTCCAATCCCTGTGGCTCTGTGTTCAGTAAGCGGCACCTTCAGAAGATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                 301 TIGGCAGIGGCIGAAAGGCAAIGCGICCCCAICIIAGCCGAIGAGAICIAGGGGACIG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T41757 347 bp mRNA EST 07-AUG-1995
10338 Lambda-PRL2 Arabidopsis thaliana cDNA clone 67A8T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
832 ctggcccagaccgccggcgccaacattctgctccccaggccaggctacccaaactacgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Jan 24, 1995 this sequence version replaced gi:634345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lansing, M.
Tel: 517-353-0854
Fax: 517-353-9168
Fmail: 22313ton@ibm.cl.msu.edu
Insert Length: 357 Std Error: 0.00
Seg primer: T7 dye primer
High quality sequence stop: 250.
Location/Qualifiers
1. 347
/organism="Narabidopsis thaliana"
/db_xref="taxon:3702"
/clone="67ABBT7"
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Arabidopsis thaliana
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T41757.1 GI:931391
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SOURCE
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grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.

8 103 t 17 others
                                                                                                                                                                                                                                                                                              994 aacaccaccgccatggtcatcataaaccccaacaaccgtgcggcagcgtttactcctac 1053
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                                                                                                                                                                                                   Gaps
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4.2%; Score 80.4; DB 23; Length 347;
Best Local Similarity 54.0%; Pred. No. 0.0001;
Matches 170; Conservative 0; Mismatches 144; Indels 1.
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ORIGIN
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